

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 6, 2004, 11:03:00 ; Search time 647 Seconds

(without alignments)  
4033.697 Million cell updates/sec

Title: US-09-837-602-2

Perfect score: 3899

Sequence: 1 MWKLLPAGGAGPEYRLLT.....KESSLADLPRYPYKRRR 754

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 2263443 seqs, 1730637950 residues

Total number of hits satisfying chosen parameters: 4526886

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh

-Q=/cgn2\_1/USPRO\_spool/US09837602/runat\_06012004\_104000\_12487/app.query.fasta\_1.903

-DB=Published Applications NA -QFWT=fastap -SUFFIX=nrnp -MINMATCH=0.1

-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100

-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0

-MAXLEN=2000000000 -USER=US09837602@cgn1.1.390 @runat\_06012004\_104000\_12487

-NCPU=6 -ICPU=3 -NO\_MMAP -LARGQUERY\_NEG\_SCORES=0 -WAIT\_DSBLBLOCK=100

-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THRSADS=1 -XGAPOP=10 -XGAPEXT=0.5

-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- Published Applications NA:
- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq\*
  - 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq\*
  - 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq\*
  - 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq\*
  - 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq\*
  - 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq\*
  - 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq\*
  - 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq\*
  - 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq\*
  - 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq\*
  - 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq\*
  - 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq\*
  - 13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq2\*
  - 14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq\*
  - 15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq\*
  - 16: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq\*
  - 17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq\*
  - 18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
-----					

c	1	416.5	10.7	475	10	US-09-917-800A-803
	2	393	10.1	272	9	US-09-923-876-5167
	3	393	10.1	272	12	US-09-923-876-5167
	4	312.5	8.0	315	10	US-09-960-352-8727
	5	227.5	5.8	6456	13	US-10-269-909-35
	6	216	5.5	442	9	US-09-864-761-11287
	7	205	5.3	114	9	US-09-864-761-27987
	8	179.5	4.6	5373	12	US-10-369-493-25273
	9	179	4.6	4437	12	US-09-801-368-51
	10	179	4.6	4437	12	US-10-369-493-45841
	11	177	4.5	5918	15	US-10-198-846-113875
	12	176	4.5	5641	13	US-10-032-585-6646
	13	174	4.5	5787	12	US-10-369-493-45712
	14	171.5	4.4	5973	13	US-10-094-466-63
	15	170.5	4.4	11167	13	US-10-252-157-188
	16	169.5	4.3	6202	13	US-10-120-988-120
	17	169.5	4.3	9555	15	US-10-084-817-244
	18	169.5	4.3	9678	15	US-10-198-846-10325
	19	167.5	4.3	7497	10	US-09-960-253-175
	20	167.5	4.3	7792	14	US-10-044-090-359
	21	166	4.3	8503	13	US-10-117-722-130
	22	166	4.3	8503	15	US-10-037-270-130
	23	165	4.2	4780	9	US-09-962-436-287
	24	165	4.2	6316	15	US-10-198-846-11287
	25	164.5	4.2	4143	12	US-10-369-493-25104
	26	164.5	4.2	5988	10	US-09-864-864-281
	27	164.5	4.2	5988	15	US-10-171-581-274
	28	164.5	4.2	6115	10	US-09-292-758-131
	29	164.5	4.2	8948	9	US-09-735-705-119
	30	164.5	4.2	8948	10	US-09-850-176A-119
	31	164.5	4.2	8948	10	US-09-897-778-119
	32	164.5	4.2	8948	11	US-09-466-396A-119
	33	164.5	4.2	8948	13	US-10-313-986-119
	34	164.5	4.2	8948	13	US-10-117-982-119
	35	164.5	4.2	9588	10	US-09-954-456-1848
	36	164.5	4.2	9588	13	US-10-393-892-32
	37	164.5	4.2	9588	13	US-10-394-382-32
	38	164.5	4.2	9588	15	US-10-146-473-1
	39	164	4.2	6297	13	US-10-311-455-967
c	40	163.5	4.2	10625	9	US-09-727-384-5
	41	163.5	4.2	10625	15	US-10-023-219-3
	42	163	4.2	7992	11	US-09-893-519A-140
	43	163	4.2	8491	13	US-10-133-013-260
	44	163	4.2	8493	14	US-10-071-766-51
	45	162.5	4.2	5857	13	US-09-873-367C-305

ALIGNMENTS

RESULT 1

US-09-917-800A-803/c

; Sequence 803, Application US/09917800A

; Patent No. US20020119462A1

; GENERAL INFORMATION:

; APPLICANT: Mendrick, Donna

; APPLICANT: Porter, Mark

; APPLICANT: Johnson, Kory

; APPLICANT: Castle, Arthur

; APPLICANT: Elashoff, Michael

; APPLICANT: Gene Logic, Inc.

; TITLE OF INVENTION: Molecular Toxicology Modeling

; FILE REFERENCE: 44921-5038-US

; CURRENT APPLICATION NUMBER: US/09/917,800A

; CURRENT FILING DATE: 2001-07-31

; PRIOR APPLICATION NUMBER: US 60/222,040

; PRIOR FILING DATE: 2000-07-31

; PRIOR APPLICATION NUMBER: US 60/222,880

; PRIOR FILING DATE: 2000-11-02

; PRIOR APPLICATION NUMBER: US 60/290,029

; PRIOR FILING DATE: 2001-05-11

; PRIOR APPLICATION NUMBER: US 60/290,645

; PRIOR FILING DATE: 2001-05-15

; PRIOR APPLICATION NUMBER: US 60/292,336

;; PRIOR FILING DATE: 2001-05-22  
;; PRIOR APPLICATION NUMBER: US 60/295,798  
;; PRIOR FILING DATE: 2001-06-06  
;; PRIOR APPLICATION NUMBER: US 60/297,457  
;; PRIOR FILING DATE: 2001-06-13  
;; PRIOR APPLICATION NUMBER: US 60/298,884  
;; PRIOR FILING DATE: 2001-06-19  
;; PRIOR APPLICATION NUMBER: US 60/303,459  
;; PRIOR FILING DATE: 2001-07-09  
;; NUMBER OF SEQ ID NOS: 1740  
;; SOFTWARE: Patent In Ver. 2.1  
;; SEQ ID NO 803  
;; LENGTH: 475  
;; TYPE: DNA  
;; ORGANISM: Rattus norvegicus  
;; FEATURE:  
;; OTHER INFORMATION: Genbank Accession No. US20020119462A1 A1137049  
US-09-917-800A-803

Alignment Scores:  
Pred. No.: 1.46e-32 Length: 475  
Score: 416.50 Matches: 82  
Percent Similarity: 83.64% Conservative: 10  
Best Local Similarity: 74.55% Mismatches: 17  
Query Match: 10.68% Indels: 1  
DB: 10 Gaps: 1

US-09-837-602-2 (1-754) x US-09-917-800A-803 (1-475)

Qy 644 GlnAspSerGluMetLeuProLysLysLeuLeuThrGluPheArgSerLeuVal 663  
|||  
Db 474 CAAGAATTCGGCAGCAGGCTTCCAGAAACTGCTGCTGACTGAATTTAGTCACTGGTT 415  
Qy 664 IleLysAsnSerThrSerArgAsnProSerGlyIleAsnAspTyrGlyGlnLeuLys 683  
|||  
Db 414 GTCCATATTAATCTCTCAGAAATCTGCGCCACTAAAT---GGTGTGGTGAATCTGAAG 359  
Qy 684 AsnPhelLysLysPheLysLysValThrTyrProGlyAlaGlyLysLeuProHisIleile 703  
|||  
Db 357 AATTTCAGAAATTCAGAAAGCTACGTCTCGAGCAGGAAAGCTTCCACACATTATT 298  
Qy 704 GlyGlySerAspLeuLeuAlaHisAlaArgLysAsnThrGluLeuGluThrLeu 723  
|||  
Db 297 GGAGATCAGATTAAATAGGTCCACATCTCGAAGAAATCTGAATTTAGAGAGTGGTTG 238  
Qy 724 ArgGlnGluMetGluValGlnAsnGlnHisAlaLysGluGluSerLeuAlaAspLeu 743  
|||  
Db 237 AACATGAATGGAGGTACAGAAACACAAACGGAAGAGACTCTCTGTGATGATCTG 178  
Qy 744 PheArgTyrAsnProTyrLeuLysArgArg 753  
|||  
Db 177 TTTAGATATAATCCTAATGTAAAAAGAAGA 148

RESULT 2  
US-09-923-876-5167  
; Sequence 5167, Application US/09923876  
; Patent No. US20020013958A1  
; GENERAL INFORMATION:  
; APPLICANT: Kamigaki, Raghunath V.  
; APPLICANT: Lalgudi, Raghunath V. (Itco)  
; APPLICANT: Sherman, Bradley K.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING  
; FILE REFERENCE: PL-0012-1 CON  
; CURRENT APPLICATION NUMBER: US/09/923,876  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: 09/298,329  
; PRIOR FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: 60/085,331  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 6332  
; SOFTWARE: PERL Program  
; SEQ ID NO 5167  
; LENGTH: 272  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030237110A9 700456477H1  
; NAME/KEY: unsure  
; LOCATION: 91, 242, 246, 256, 258, 260, 267, 270  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-923-876-5167

Alignment Scores:  
Pred. No.: 1.47e-30 Length: 272  
Score: 393.00 Matches: 77

;; TYPE: DNA  
;; ORGANISM: Zea mays  
;; FEATURE:  
;; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700456477H1  
; NAME/KEY: unsure  
; LOCATION: 91, 242, 246, 256, 258, 260, 267, 270  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-923-876-5167

Alignment Scores:  
Pred. No.: 1.47e-30 Length: 272  
Score: 393.00 Matches: 77  
Percent Similarity: 96.30% Conservative: 1  
Best Local Similarity: 95.06% Mismatches: 3  
Query Match: 10.08% Indels: 0  
DB: 9 Gaps: 0

US-09-837-602-2 (1-754) x US-09-923-876-5167 (1-272)

Qy 469 AspGluGluAsnGlnGluMetSerSerCysLysSerAlaArgIleGluThrSerCysSer 488  
|||  
Db 3 GATGAAGAAATCAAGAAATGCTTTCATGCAAAATCAGCAAGAAATAGAAACGCTCTGTCT 62  
Qy 489 LeuLeuGluGlnThrGlnProAlaThrProSerLeuTyrLysAsnLysGluGlnHisLeu 508  
|||  
Db 63 CTTTGAACAAACACACACCTGCTACACNCTCATTTGTGNAATAATAGGAGCAGCATCTA 122  
Qy 509 SerGluAsnGluProValAspThrAsnSerAspAsnAsnLeuPheThrAspThrAspLeu 528  
|||  
Db 123 TCTGAGAATGAGCTGTGGACACAAACTCAGACAATAACTTATTACAGATACAGATTTA 182  
Qy 529 LysSerIleValLysAsnSerAlaSerLysSerHisAlaGluLysLeuArgSerAsn 548  
|||  
Db 183 AATCTATTGTGAAAAATCTGCCAGTAAATCTCATGCTGCAGAAAGCTAAAAAAN 242  
Qy 549 Lys 549  
|||  
Db 243 AAA 245

RESULT 3  
US-09-923-876-5167  
; Sequence 5167, Application US/09923876  
; Publication No. US20030237110A9  
; GENERAL INFORMATION:  
; APPLICANT: Kamigaki, Raghunath V.  
; APPLICANT: Lalgudi, Raghunath V. (Itco)  
; APPLICANT: Sherman, Bradley K.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING  
; FILE REFERENCE: PL-0012-1 CON  
; CURRENT APPLICATION NUMBER: US/09/923,876  
; CURRENT FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: 09/298,329  
; PRIOR FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: 60/085,331  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 6332  
; SOFTWARE: PERL Program  
; SEQ ID NO 5167  
; LENGTH: 272  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030237110A9 700456477H1  
; NAME/KEY: unsure  
; LOCATION: 91, 242, 246, 256, 258, 260, 267, 270  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-923-876-5167

Alignment Scores:  
Pred. No.: 1.47e-30 Length: 272  
Score: 393.00 Matches: 77

BEST AVAILABLE COPY









; APPLICANT: Hecht, Peter  
 ; APPLICANT: Holtzman, Doug  
 ; APPLICANT: Madden, Kevin  
 ; APPLICANT: Maxon, Mary  
 ; APPLICANT: Milne, Todd  
 ; APPLICANT: No. US20020128250Alman, Thea  
 ; APPLICANT: Royer, John  
 ; APPLICANT: Salama, Sofie  
 ; APPLICANT: Sherman, Amir  
 ; APPLICANT: Silva, Jeff  
 ; APPLICANT: Summers, Eric  
 ; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi  
 ; FILE REFERENCE: 109272.147  
 ; CURRENT APPLICATION NUMBER: US/09/801,368  
 ; PRIOR FILING DATE: 2001-03-07  
 ; PRIOR APPLICATION NUMBER: US 09/487,558  
 ; PRIOR FILING DATE: 2000-01-19  
 ; PRIOR APPLICATION NUMBER: US 60/160,587  
 ; PRIOR FILING DATE: 1999-10-20  
 ; NUMBER OF SEQ ID NOS: 440  
 ; SOFTWARE: Patent in version 3.0  
 ; SEQ ID NO 51  
 ; LENGTH: 4437  
 ; TYPE: DNA  
 ; ORGANISM: Saccharomyces cerevisiae  
 ; US-09-801-368-51

Alignment Scores:  
 Pred. No.: 3,36e-07 Length: 4437  
 Score: 179,00 Matches: 108  
 Percent Similarity: 38.92% Conservativeness: 87  
 Best Local Similarity: 21.56% Mismatches: 167  
 Query Match: 4.59% Indels: 139  
 DB: 10 Gaps: 21

US-09-837-602-2 (1-754) x US-09-801-368-51 (1-4437)

QY 324 AspProGlnGlyHisProSerThrGlyLeuLysThrThrProGlyProSerLeuSer 343  
 DB 1156 AATCCACAAGTGCAT-----AGTCTGTCTAGTGAATAATTTAGCT 1194  
 QY 344 GlnGlyValSerValAspGluLysLeuMetProSerAlaProValAsnThrThrThrTyr 363  
 DB 1195 AAAGGAAATCTAAACACTATGAACCTAAATGTCTTCACTTTAAACAACTCTCA-- 1251  
 QY 364 ValAlaAspThrGluSerGluGlnAlaAspThrTrpAspLeuSerGluArgProLysGlu 383  
 DB 1252 ---CTACCCACTCGGATGATAAAGGTAAATTTATGGTAATAATCAAAAGAGAGCCAA 1308  
 QY 384 IleLysValSerLysMetGluGlnLysPheArgMetLeuSerGlnAspAlaProThrVal 403  
 DB 1309 ATAGGGGTTCTAGCCCCAATACGGTAGCTTATGTAACGCTCAAGAAACTCCATCCTTA 1368  
 QY 404 LysGluSerCysLysThrSerSerAsnAsnSerMetValSerAsnThrLeuAlaLys 423  
 DB 1369 AAA-----TCGAATTCGAGTACTGCTACCTTAACCGTACAAACGGCAGAT 1413  
 QY 424 MetArgIleProAsnTyrGlnLeuSerProThrLysLeuProSerIleAsnLysSerLys 443  
 DB 1414 GTAATAATACATCTCCATCTTCATCACA-----CGCCAATACCCCAAACTGCA 1464  
 QY 444 AspArgAlaSerGlnGlnGlnGlnThrAsnSerIleArgAsnTyrPheGlnProSerThr 463  
 DB 1465 AACAGAAGTTTGGAGGTTCATCAGCACA----- 1491  
 QY 464 LysLysArgGluArgAspGluGluAsnGlnGluMetSerSerCysLysSerAlaArgIle 483  
 DB 1492 -----GAAGATACACCTAAATAATTTCTTCAACACCGGGTCTTTTAAA 1533  
 QY 484 GluThr-----SerCysSerLeuLeuGluGlnThrGlnProAlaThrProSerLeuTrp 501  
 DB 1534 GAACAGTATCCTGATTGTATTATTAATCCAGACAAGACAGTTCAGTCGGCGGTAATAATCA 1593

# RESULT 10

US-10-369-493-45841  
 ; Sequence 45841, Application US/10369493  
 ; Publication No. US20030233675A1  
 ; GENERAL INFORMATION:

QY 502 LysAsnLysGluGlnHisLeu----- 508  
 DB 1594 AAGTATAGTGTAAAGAACTTTTATCTGGACCAAAATTTTATCTCTGAAGAAACAGGG 1653  
 QY 509 -----SerGluAsnGluProValAspThrAsnSerAspAsnLeuPheThrAsp 525  
 DB 1654 TTAATGATAGTAGAATAAATATATTTCTGGTTACCAAGAGATATGTAGTTTGTTCGG 1713  
 QY 526 ThrAspLeuLysSerIleValLysAsnSerAlaSerLysSerHisAlaAlaGluLysLeu 545  
 DB 1714 CTAAACTTAAAGAGTAGCAAAATTTATCCAGTTTCAAGAACTCTCTCACAAATTTG 1773  
 QY 546 ArgSerAsnLysLysArg-----GluMetAspAsp-----Val 556  
 DB 1774 GGAATCAATCACAAAAATGTCACTTTCCATATGACAGACTTTGATTCGGATATTGGTGT 1833  
 QY 557 AlaIleGluAspGluValLeuGlu-----GlnLeuPheLysAspThrLysPro 572  
 DB 1834 GCAATTCAGATGATCTTTGGAAATTTTGAAGAAAGCTTGTTTTTGAACACTTCTGGA 1893  
 QY 573 GluLeuGluIle-----AspValLysValGlnLysGln----- 583  
 DB 1894 AAAATTTATATCAAGACCAAAATGAAGCTTCAACAAACCGAACCTGCTCTCTCACC 1953  
 QY 584 ---GluGluAspVal-----AsnValArgLysArgProArgMetAspIleGluThr 599  
 DB 1954 TCAGAAACCAATGTCTTTTAAATCGGTGAAAGTAAGAGTTCAATGAGGTCCGGAACA 2013  
 QY 600 AsnAspThrPheSerAsp-----GluAlaValProGluSerSerLysIleSer 615  
 DB 2014 AGCAGTCTGATAGCATCGACAGATGATGTTTCCATTTGCTACTGCTCTTCGACATAACA 2073  
 QY 616 GlnGluAsnGlu----- 619  
 DB 2074 TCATTTGATGAACATGCATCAGGAAGTGGCGGAGGTACCCCAACCCCGAGTTATTAC 2133  
 QY 620 -----IleGlyLysLysArgGluLeuLysGluAspSerLeuTrpSerAlaLysGlu 636  
 DB 2134 TATGACAGAGTTTCCAATACTAATCCAACCTGAAGAAATTTGAATTTATTTGAAATATTAAAGAA 2193  
 QY 637 IleSerAsnAsnAspLysLysLeuGlnAspAspSerGluMetLeuProLysLysLeuLeu 656  
 DB 2194 GTTCTTTCATCAG-----GAAATATGCACCAAAATTTGTTTAA 2235  
 QY 657 ThrGluPheArg-----SerLeuValIleLysAsnSerThrSerArgAsnProSer 673  
 DB 2236 ACAAGTCCAAATTAGAATCAACCTACAGATTAAGGAAGTAAATTAATATTCTCTACC 2295  
 QY 674 GlyIleAsnAspAspTyrGlyGlnLeuLysAsnPheLysLysPheLysValThrTyr 693  
 DB 2296 CCATAACAGAAATGAAGCAAG---AGTAGTTTTCAAGTGTCTAAGAAAA----- 2343  
 QY 694 ProGlyAlaGlyLysLeuProHisIleIleGlyLysSerAspLeuIleAlaHisAla 713  
 DB 2343 ----- 2343  
 QY 714 ArgLysAsnThrGluLeuGluTrpLeuArgGlnGlnMetGlu-ValGlnAsnGln-- 732  
 DB 2344 GATGAGGGAGCTGAATTTGATTTCAATCATCTGATGGAATCGCTTATACAAACCAAGAA 2403  
 QY 733 ----HisAlaLysGluGlu-----SerLeuAlaAspAspLeuPheArgTyrAsnProTyr 749  
 DB 2404 CTGGCACCAAAAGAGAGAGCTCCCAAGCTCCCGCAAAATACTTCTCTCAGAGACCTTA 2463  
 QY 749 r 749  
 DB 2464 T 2464

APPLICANT: Cao, Yongwei  
 APPLICANT: Hinkle, Gregory J.  
 APPLICANT: Slater, Steven C.  
 APPLICANT: Goldman, Barry S.  
 APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
 FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493  
 CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039  
 PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 45841

LENGTH: 4437

TYPE: DNA

ORGANISM: Saccharomyces cerevisiae

US-10-369-493-45841

Alignment Scores:  
 Pred. No.: 3.36e-07 Length: 4437  
 Score: 179.00 Matches: 108  
 Percent Similarity: 38.92% Conservatives: 87  
 Best Local Similarity: 21.56% Mismatches: 167  
 Query Match: 4.59% Indels: 139  
 DB: 12 Gaps: 21

US-09-837-602-2 (1-754) x US-10-369-493-45841 (1-4437)

QY 324 AsproGlnGlyHisProSerThrGlyLeuLysThrThrProGlyProSerLeuSer 343  
 DB 1156 AATCCCAAGGTCTAT-----AGTCTGTCTAGTGAATTTAGCT 1194  
 QY 344 GlnGlyValSerValAspGluLysLeuMetProSerAlaProValAenThrThrTyr 363  
 DB 1195 AAGGAAATCTAACTAATGTAATTTATGGAATAATTTCAAAAGAGAGCCAA 1251  
 QY 364 ValAlaAspThrGluSerGluGlnAlaAspThrTyrAspLeuSerGluArgProLysGlu 383  
 DB 1252 ---CTACCACCTCGGATGATAAGGTAATTTATGGAATAATTTCAAAAGAGAGCCAA 1308  
 QY 384 IleLysValSerLysMetGluGlnLysPheArgMetLeuSerGlnAspAlaProThrVal 403  
 DB 1309 ATAGGGTCTCTACCCCAATACGGTAGCTTATGTAACGCTCTCAAGAACTCCATCCTTA 1368  
 QY 404 LysGluSerCysLysThrSerSerAsnAsnSerMetValSerAsnThrLeuAlaLys 423  
 DB 1369 AAA-----TGAATTCGAGTACTGTACTTACCTTAACCGTACAAACGGCAGAT 1413  
 QY 424 MetArgIleProAsnThrGlnLeuSerProThrLysLeuProSerIleAsnLysSerLys 443  
 DB 1414 GTAATATACCATCTCCATCTTCATCACC-----CGCCCAATACCCAAACTGCA 1464  
 QY 444 AspArgAlaSerGlnGlnGlnThrAsnSerIleArgAsnThrPheGlnProSerThr 463  
 DB 1465 AACAGAGTGTGGAGGTTCATCAGACA-----1491  
 QY 464 LysLysArgGluArgAspGluGlnGlnGlnMetSerSerCysLysSerAlaArgIle 483  
 DB 1492 -----GAAGATACACCTTAATTTCTTCAACCGCGGTCTTTAAA 1533  
 QY 484 GluThr-----SerCysSerLeuLeuGluGlnThrGlnProAlaThrProSerLeuTrp 501  
 DB 1534 GAAACGTATCTGATTTGATTAATCCAGACAAGAGAGTTCAGTCCGGTAAATAATCAA 1593  
 QY 502 LysAsnLysGluGlnHisLeu-----508  
 DB 1594 AAGTATAGTGAAGAACTTTTACTCGACCAAAATTTTATCTCTGAAGAAACAGGG 1653  
 QY 509 -----SerGluAsnGluProValAspThrAsnSerAspAsnLeuPheThrAsp 525  
 DB 1654 TTAATCATAGTGAAGATAATATATTTCTGGTACCAGAAAGATATGTTAGTTTGTCCG 1713

QY 526 ThrAspLeuLysSerIleValLysAsnSerAlaSerLysSerHisAlaAlaGluLysLeu 545  
 DB 1714 CTAACCTTAAAGAGTGTAGCAAAATATCCAGTTTCAAGAAATCTGCTCTCACAAATTTG 1773  
 QY 546 ArgSerAsnLysLysArg-----GluMetAspAsp-----Val 556  
 DB 1774 GGAATCAATCACAAAAATGTCACTTTTCCATATGACAGACTTTTGATTCGATATTTGGTGTCT 1833  
 QY 557 AlaIleGluAspGluValLeuGlu-----GlnLeuPheLysAspThrLysPro 572  
 DB 1834 GCAATTCAGATGATACTTTGGAAATTTTGAATAAAGAGCTTTGTTTGAACACTTCTCGGA 1893  
 QY 573 GluLeuGluIle-----AspValLysValGlnLysGln-----583  
 DB 1894 AAAATTTATATCAAGACCAAAATGAAGCTTCAACAAAACCGAAACCTGCTCTCTCAC 1953  
 QY 584 ---GluGluAspVal-----AsnValArgLysArgProArgMetAspIleGluThr 599  
 DB 1954 TCAGAAAACAATGTTCTTTTAAATCGTGAAAGTAAGAGTTTCAATGAGGTCCGGAACA 2013  
 QY 600 AsnAspThrPheSerAsp-----GluAlaValProGluSerSerLysLysLeu 615  
 DB 2014 AGCAGTCTGATGATCGACAGATGATGTTTCCATTTGTCACCTCGTCTTCTGACATAACA 2073  
 QY 616 GlnGluAsnGlu-----619  
 DB 2074 TCATTTTGATGAACATCATCAGGAAGTGGCGCAGGTACCCCAACCCGAGTTATTAC 2133  
 QY 620 -----IleGlyLysLysArgGluLeuLysGluAspSerLeuTrpSerAlaLysGlu 636  
 DB 2134 TATGACAGAGTTTCCAAATACTAATCAACTGGAAGAAATTTGAATATTGAATATTAAAGAA 2193  
 QY 637 IleSerAsnAsnAspLysLeuGlnAspSerGluMetLeuProLysLysLysLeuLeu 656  
 DB 2194 GTTCTTTTCATGAG-----GAAATGCACCAAAATGGTTTTTAAA 2235  
 QY 657 ThrGluPheArg-----SerLeuValIleLysAsnSerThrSerArgAsnProSer 673  
 DB 2236 ACAAGTCCAAATTAGAATCTCAACCTACAGATAAAGGAAGTAAATTAATATTCTCTACC 2295  
 QY 674 GlyIleAsnAspAspTyrGlyGlnLeuLysAsnPheLysLysPheLysLysValThrTyr 693  
 DB 2296 CCATTAACAGAAATGAAGCAAG---AGTAGTTTTTCAAGTCTGAAGAAA-----2343  
 QY 694 ProGlyAlaGlyLysLeuProHisIleGlySerAspLeuIleAlaHisAla 713  
 DB 2343 -----2343  
 QY 714 ArgLysAsnThrGluLeuGluTrpLeuArgGlnGluMetGlu-ValGlnAsnGln-- 732  
 DB 2344 GATGAGGGACTGAAATTTGATTTCAATCATCGTAGGGAATCGGCTTATACAAAACCCAGAA 2403  
 QY 733 ---HisAlaLysGluGlu-----SerLeuAlaAspAspLeuPheArgTyrAsnProTyr 749  
 DB 2404 CTGGCACCACCAAGAGAGAGCTCCCAAGCTCCCGCAAAATCTTCTCTCAGAGACCTTA 2463  
 QY 749 r 749  
 DB 2464 T 2464

# RESULT 11

US-10-198-846-13875  
 ; Sequence 13875, Application US/10198846  
 ; Publication No. US20030059974A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lillie, James  
 ; APPLICANT: Xu, Yongyao  
 ; APPLICANT: Wang, Youzhen  
 ; APPLICANT: Steinmann, Kathleen  
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
 ; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
 ; TITLE OF INVENTION: THERAPY OF BREAST CANCER  
 ; FILE REFERENCE: MRI-049



## BEST AVAILABLE COPY

```

; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13875
; LENGTH: 5918
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-846-13875

```

Alignment Scores:	
Pred. No.:	8.23e-07
Score:	177.00
Percent Similarity:	34.9%
Best Local Similarity:	20.9%
Query Match:	4.54%
DB:	15
	Gaps: 41
	Indels: 313
	Mismatches: 267
	Conservative: 125
	Matches: 187
	Length: 5918

US-09-837-602-2 (1-754) x US-10-198-846-13875 (1-5918)

Qy	17	ArgLeuLeuThrGlyValGluTyrValValGlyArgLysAsnCysAlaIleLeuLeuGlu	36
Db	1242	CGGGTGAAGGTGGGTAAACGAGTATGTCCACCAAGGGGCAGAGTGTACACGAGGTGTACTAT	1301
Qy	37	AsnAspGlnSerIleSerArgAsnHisAlaValLeuThrAlaAsnPheSerValThrAsn	56
Db	1302	TCCATCGGGGACCTGGCCAAAGTCAGTGTACGAGAAGATGTTCAACTCGATGGTGGACACGC	1361
Qy	57	LeuSerGlnThrAspGlu	68
Db	1362	ATCAACGACCAACCTGGAGACCAACGACGCCAGCCAGTCATTTCATAGGTGTCTGGACATC	1421
Qy	69	LysAsp	80
Db	1422	GCCGGCTTTGAGATCTTTGATTTTCAACAGCTTTGAGCAGCTGTGTCATCAACTTCACCAAT	1481
Qy	81	GluLysMetGlnAsnGlyPheSerArgThrLeu	91
Db	1482	GAGAACTCGAGCAGTCTTCAACACCACCATGTTCTGCTGGAGCAGGAGAGTACAAG	1541
Qy	92	LysSerGlyAspGlyIleThrPheGlyValPheGlySerLysPheArgIleGluTyrGlu	111
Db	1542	AAGGAAGGCATCGAGTGCAGCTTTATTCAGCTTCGGCATGGACCTGCAG	1589
Qy	112	ProLeuValAlaCysSerSerCysLeuAspValSerGlyLysThrAlaLeuAsnGlnAla	131
Db	1590	-----GCTGTCATCGACCTCATCGAAGGCCATCGAGGCCATGGGCATCATGTCC	1631
Qy	132	IleLeuGlnLeuGlyGlyPheThrValAsnAsnTrpThrGluGluCysThrHisLeuVal	151
Db	1632	ATCCTGAG-----GAGGAGTGC-----	1649
Qy	152	MetValSerValLysValThrIleLysThrIleCysAlaLeuIleCysGlyArgProIle	171
Db	1650	----ATGTTCCTCCCAAGGCCACGGACATGACCTTCAAGGCCAAGCTGTACGACCAACCACCTG	1706
Qy	172	ValLysProGluTyrPheThrGluPheLeuLysAlaValGlnSerLysLysGlnPro	190
Db	1707	GGCAAGTCCAAACAATTTCCAGNAG---CCTCGCAATGTCAAGGGGAAGCAGGAAAGCCAC	1763
Qy	191	-----ProGlnIleGluSer	195
Db	1764	TTTCTCTGTTCCACTATGTCGCACCGTGGACTACAACATCTTTGGCTGGCTGGGAAG	1823
Qy	196	PheTyrProProLeuAspGluProSerIleGly	212
Db	1824	AACAAGACCTCTCAACGAGACGGTGGTGGGGCTGTACCAAGAGTCTCTCCCTCAAACTC	1883
Qy	213	-----SerGlyArg	215
Db	1884	ATGCCCACTCTTCTCCACCTATGCTTCTGCTGATACCGGTGACAGTGGGAAGGCAGA	1943

## BEST AVAILABLE COPY

Qy 488 Ser----LeuLeuGluGlnThrGlnProAlaThrProSerLeuTrpLys----AsnLysGlu 505  
Db 2880 TCAGAGCTCAAGAAAGATATCGATGACCTGGAGCTGACCCCTGGCCAAAGGTGGGAAGGAA 2939  
Qy 506 GlnHisLeuSerGluAenGluProValAspThrAsnSerAspAsnAenLeuPheThrAsp 525  
Db 2940 AAGCACCAACAGAGAACAAG----- 2960  
Qy 526 ThrAspLeuLysSerIleValLysAenSerAlaSerLysSerHisAlaAlaGluLysLeu 545  
Db 2961 -----GTTAAAAACCTGCAGAGGAGATGGCCGGCTGCACGAGATCATTTGCCAAGCTG 3014  
Qy 546 ArgSerAsnLysLys-----ArgGluMetAspAspValAlaIle 558  
Db 3015 ACCAAGAGGAGAAAGCTCTTCAAGAGGCCCCACGACCAAGCCCTAGTAGACCTTACGGCT 3074  
Qy 559 GluAspGluValLeuGluGlnLeuPheLysAspThrLysProGluLeuGluIleAspVal 578  
Db 3075 GAGGAACAAAGGTCAACACACTG-----ACCAAGTCTAAAGTCAAGCTGGAGCAG 3125  
Qy 579 LysValGlnLysGlnGluAspValAsnValArgLysArgProArgMetAspIleGlu 598  
Db 3126 CAGGTGATGATCTGGAGGATCCCTGGAGCAGAGAAGGTGCCATGTCGACCTGGAG 3185  
Qy 599 ThrAsnAspThrPheSerAspGluAlaValProGluSerSerLysIleSerGlnGluAsn 618  
Db 3186 CGA----- 3188  
Qy 619 GluIleGlyLysLysArgGluLeuLysGluAspSerLeuTrpSerAlaLysGluIleSer 638  
Db 3189 -----GCAAAGCGGAACCTGGAGGTTGACCTGAAGCTGACCCAGGAGAGCATCATG 3239  
Qy 639 Asn-----AsnAspLysLeuGlnAspAspSerGluMetLeuProLysLysLeuLeuLeu 656  
Db 3240 GACCTGGAGAACGACAAGACTTCAG-----CTGAGGAGAAAAGCTCAAGAAG 3284  
Qy 657 ThrGluPheArgSerLeuValIleLysAsnSerThrSerArgAenProSerGlyIleAsn 676  
Db 3285 AAAGAGTTT-----GACATCAGTCAGACGACAGCACTAAATATAGAG 3323  
Qy 677 AspAspTyrGly----GlnLeuLysAenPheLysLysPheLysLysValThrTyrProGly 695  
Db 3324 GATGAGCAGGCCCTGGCCCTTCAGCTGCAGAAGAACTGAAGGAA----- 3368  
Qy 696 AlaGlyLysLeuProHisIleIleGlyGlySerAspLeuIleAlaHisAlaArgLys 715  
Db 3369 -----AAACGAGGCACGC 3380  
Qy 716 AsnThrGluLeuGluTyrLeuArgGlnGlnMetGluValGlnAenGlnHisAlaLys 735  
Db 3381 ATCCAGAGACTGGAGGAGGACTAGAGCCGAG-----CCGACAGCCCGGCCCAAG 3431  
Qy 736 GluGluSerLeuAlaAspAspLeuPheArg 745  
Db 3432 GTGAGAAAGCTGCCTCAGACCTGACCCGG 3461









GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 6, 2004, 10:40:04 ; Search time 127 Seconds  
(without alignments)  
2620.495 Million cell updates/sec

Title: US-09-837-602-2  
Perfect score: 3899  
Sequence: 1 MWKLLPAGGAGGEPVRLLT.....KEESLADDLFRYPNPKRRR 754

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgn2\_1/uspto.spool/US09837602/runat 06012004 103959 12455/app query.fasta\_1.903  
-DB=Issued\_Patents\_NA -QWTF=fastap -SUFFIX=rni -MINMATCH=0.1 -LOEPCI=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09837602 @CGN 1 1 56 @runat 06012004 103959 12455 -NCPU=6 -ICPU=3  
-NO.MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:

- 1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq:\*\*
- 2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*\*
- 3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq:\*\*
- 4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq:\*\*
- 5: /cgn2\_6/ptodata/1/ina/6CTUS.COMB.seq:\*\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3896	99.9	4386	US-09-300-008B-1	Sequence 1, Appli
2	175	4.5	5661	US-08-938-105-2	Sequence 2, Appli
3	169	4.3	3384	US-08-923-992A-5	Sequence 5, Appli
4	166	4.3	8503	US-09-620-312D-130	Sequence 130, App
5	164.5	4.2	8948	US-09-643-597-119	Sequence 119, App
6	164.5	4.2	8948	US-09-480-884A-119	Sequence 119, App
7	164.5	4.2	8948	US-09-542-615A-119	Sequence 119, App
8	164.5	4.2	8948	US-09-606-421B-119	Sequence 119, App
9	163	4.2	8257	US-09-595-684B-30	Sequence 30, Appl
10	162.5	4.2	5857	US-09-220-132-79	Sequence 79, Appl
11	162	4.2	3135	US-09-107-532A-1575	Sequence 1575, Ap
12	161	4.1	3294	US-08-923-992A-7	Sequence 7, Appli

13	157.5	4.0	2672	3	US-09-214-564A-5	Sequence 5, Appli
14	157.5	4.0	2815	3	US-09-214-564A-1	Sequence 1, Appli
15	157	4.0	4200	1	US-08-242-932-1	Sequence 1, Appli
16	157	4.0	4200	1	US-08-714-481-1	Sequence 1, Appli
17	157	4.0	4200	5	PCT-US95-06111-1	Sequence 1, Appli
18	157	4.0	4200	5	US-08-923-992A-1	Sequence 1, Appli
19	156.5	4.0	3393	3	US-09-104-324B-1	Sequence 1, Appli
20	156.5	4.0	3393	3	US-09-162-713-1	Sequence 1, Appli
21	156	4.0	3492	3	US-08-923-992A-9	Sequence 9, Appli
22	155.5	4.0	1704	2	US-08-630-822A-67	Sequence 67, Appl
23	155.5	4.0	1704	2	US-09-005-069-67	Sequence 67, Appl
24	155.5	4.0	1704	4	US-09-171-156A-26	Sequence 26, Appl
25	155.5	4.0	1704	4	US-09-004-730A-26	Sequence 26, Appl
26	155.5	4.0	1704	4	US-08-981-799A-26	Sequence 26, Appl
27	155	4.0	30549	4	US-09-134-001C-322	Sequence 322, App
28	154.5	4.0	6755	3	US-08-931-999-4	Sequence 4, Appli
29	151	3.9	1830121	4	US-09-557-884-1	Sequence 1, Appli
30	151	3.9	1830121	4	US-09-643-990A-1	Sequence 1, Appli
31	150.5	3.9	3063	4	US-08-294-312B-3	Sequence 3, Appli
32	150.5	3.9	3063	4	US-08-468-024B-3	Sequence 3, Appli
33	150.5	3.9	3063	4	US-09-708-200-12	Sequence 12, Appl
34	150.5	3.9	5194	2	US-09-599-652-1	Sequence 1, Appli
35	150.5	3.9	5194	2	US-08-642-846-1	Sequence 1, Appli
36	150.5	3.9	5194	4	US-09-264-604-1	Sequence 1, Appli
37	150	3.8	1383	2	US-08-630-822A-82	Sequence 82, Appl
38	150	3.8	1383	2	US-09-005-069-82	Sequence 82, Appl
39	150	3.8	1383	4	US-09-171-156A-28	Sequence 28, Appl
40	150	3.8	1383	4	US-09-004-730A-28	Sequence 28, Appl
41	150	3.8	1383	4	US-08-981-799A-28	Sequence 28, Appl
42	149.5	3.8	2617	1	US-08-430-024-1	Sequence 1, Appli
43	149.5	3.8	2617	1	US-08-782-009-1	Sequence 1, Appli
44	149.5	3.8	2617	3	US-09-017-302-1	Sequence 1, Appli
45	147.5	3.8	3730	1	US-08-242-932-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-09-300-008B-1  
; Sequence 1, Application US/09300008B  
; Patent No. 6458534  
; GENERAL INFORMATION:  
; APPLICANT: Concannon et al.  
; TITLE OF INVENTION: A GENE ASSOCIATED WITH NIJMEGEN BREAKAGE  
; FILE REFERENCE: 9924-0003-228  
; CURRENT APPLICATION NUMBER: US/09/300,008B  
; CURRENT FILING DATE: 1999-04-27  
; PRIOR APPLICATION NUMBER: US 60/083,269  
; PRIOR FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 4386  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (26)...(2287)  
US-09-300-008B-1

Alignment Scores:  
Pred. NO.: 0  
Score: 3896.00  
Percent Similarity: 100.00%  
Best Local Similarity: 99.87%  
Query Match: 99.92%  
DB: 4  
Length: 4386  
Matches: 753  
Conservative: 1  
Mismatch: 0  
Indels: 0  
Gaps: 0

US-09-837-602-2 (1-754) x US-09-300-008B-1 (1-4386)

Qy 1 MetTPrpYsLeuLeuProAlaAagGlyProAlaGlyGlyGluProTyrArgLeuThr 20

**THIS PAGE BLANK (100%)**



Db 26 ATGTGAAACTGCTGCCCGCGCGCGCGAGGAGGAGAACCATACAGACTTTTGACT 85  
Qy 21 GlyValGluThrValValGlyArgLysAsnCyAlaIleLeuIleGluAsnAspGlnSer 40  
Db 86 GCGGTGTAGTACCTGTTGTGAAGGAAACCTGCGCAATCTGATTGAAATGATCAGTCG 145  
Qy 41 IleSerArgAsnHisAlaValLeuThrAlaAsnPheSerValThrAsnLeuSerGlnThr 60  
Db 146 ATCAGCCGAATCATGCTGTGTACTGCTTAACTTTCTGTAAACCACTGAGTCAACA 205  
Qy 61 AspGluIleProValLeuThrLeuLysAspAsnSerLysThrGlyThrPheValAsnGlu 80  
Db 206 GATGAATCCCTGATTGACATTAAGAGATAATCTTAAGTATGATGATGATGATGATG 265  
Qy 81 GluLysMetGlnAsnGlyPheSerArgThrLeuLysSerGlyAspGlyIleThrPheGly 100  
Db 266 GAAATAATGAGANTGCTTTTCCCGAAGCTTTGAAAGTGGGGGATGATGATGATGATG 325  
Qy 101 ValPheGlySerLysPheArgIleGluThrGluProLeuValAlaCysSerSerCysLeu 120  
Db 326 GTGTTTGGAGAGTAAATTCAGATAGAGTATGAGCTTTTGGTTCATGCTCTTCTGTGTTA 385  
Qy 121 AspValSerGlyLysThrAlaLeuAsnGlnAlaIleLeuGlnLeuGlyGlyPheThrVal 140  
Db 386 GATGCTCTCTGGGAAACTGCTTTAAATCAAGCTATATTCAGCTATATTCAGCTGATG 445  
Qy 141 AsnAsnTrpThrGluGluCysThrHisLeuValMetValSerValLysValThrIleLys 160  
Db 446 AACATTTGACAGAGAGATGCTACCTTTGTCATGATATCATGATGATGATGATGATG 505  
Qy 161 ThrIleCysAlaLeuIleCysGlyArgProIleValLysProGluThrPheThrGluPhe 180  
Db 506 ACAATATGTGCACTATTGTGAGCTCCAAATTTGTAAGCCAGATATTTTACTGAAATC 565  
Qy 181 LeuLysAlaValGlnSerLysLysGlnProProGlnIleGluSerPheThrProLeu 200  
Db 566 CTGAAGAGCTGTGAGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 625  
Qy 201 AspGluProSerIleGlySerLysAsnValAspLeuSerGlyArgGlnGluArgLysGln 220  
Db 626 GATGAACCATCTATTGGAAGTAAATAATGTTGATCTGTGAGGAGCGGAGAGAGAGAA 685  
Qy 221 IlePheLysGlyLysThrPheLeuAsnAlaLysGlnHisLysLysLysLeuSerSer 240  
Db 686 ATCTTCAAGAGGAGAAACATTTATATTTTGAATGCCAAGACATTAAGAAATTTGATTC 745  
Qy 241 AlaValValPheGlyGlyGlyGluAlaArgLeuIleThrGluGluAsnGluGluHis 260  
Db 746 GCAGTTGCTTTTGGAGGTGGGAGAGCTAGTTGATAACAGAGAGAGAGAGAGAGAGAG 805  
Qy 261 AsnPhePheLeuAlaProGlyThrCysValValAspThrGlyIleThrAsnSerGlnThr 280  
Db 806 AATTTCTTTTGGCTCCGGGACGTGTGTTGTTGATACAGGAATTAACAACTCACAGACC 865  
Qy 281 LeuIleProAspCysGlnLysLysTrpIleGlnSerIleMetAspMetLeuGlnArgGln 300  
Db 866 TTAATTTCTGACTGTGAG 925  
Qy 301 GlyLeuArgProIleProGluAlaGluIleGlyLeuAlaValIlePheMetThrThrLys 320  
Db 926 GGTCTTAGACCTTATTCCTGAAGCAGAAATTTGATTTGGGGGTGATTTTTCATGACTACA 985  
Qy 321 AsnTrpCysAspProGlnGlyHisProSerThrGlyLeuLysThrThrProGlyPro 340  
Db 986 AATTAATCTGATCCTCAGGGCCATCCAGTACAGATTAAGAGCAACCACTCCAGAGCA 1045  
Qy 341 SerLeuSerGlnGlyValSerValAspGluLysLeuMetProSerAlaProValAsnThr 360  
Db 1046 AGCCTTTTCAAGAGGGGTGCTGATGATGAATAACTTAATGCCAGAGCGCCCGAGTGA 1105  
Qy 361 ThrThrTrpValAlaAspThrGluSerGluGlnAlaAspThrTrpAspLeuSerGluArg 380  
Db 1106 ACACATAGTAGTGACACAGATCAGAGCAGCAGATACATGCGGATTTGATGAGAGAG 1165

Qy 381 ProLysGluIleLysValSerLysMetGluGlnLysPheArgMetLeuSerGlnAspAla 400  
Db 1166 CCAAAAGAAATCAAGAGTCTCCAAAATGGAACAAAATTCAGAAATGCTTTTCACAGATGCA 1225  
Qy 401 ProThrValLysGluSerCysLysThrSerSerAsnAsnAsnSerMetValSerAsnThr 420  
Db 1226 CCCACTGTAAAGAGGAGTCTCTGCAAAACAGAGCTCTAATAATAATAGTATGATGATCAATACT 1285  
Qy 421 LeuAlaLysMetArgIleProAsnTrpGlnLeuSerProThrLysLeuProSerIleAsn 440  
Db 1286 TTGGCTAAGATGAGATCCCAAACTATCAGGCTTTCCACCACCTAATATCCCAAGTATAAAT 1345  
Qy 441 LysSerLysAspArgAlaSerGlnGlnGlnThrAsnSerIleArgAsnTrpPheGln 460  
Db 1346 AAAAGTAAAGATAGGGCTTCTCAGCAGCAGCAGACCACTCCATCAGAAAATCTACTTTTCAG 1405  
Qy 461 ProSerThrLysLysArgGluArgAspGluAsnGlnGluMetSerSerCysLysSer 480  
Db 1406 CCGTCTCAAAAAGAGGAGGAGGATCAAGAAAATCAAGAAAATGTCTTTCATGCAAAATCA 1465  
Qy 481 AlaArgIleGluThrSerCysSerLeuLeuGluGlnThrGlnProAlaThrProSerLeu 500  
Db 1466 GCAAGAATAGAAACGTCTTGTCTCTTTTAGAACCAACCAACCTGCTACACCTCATG 1525  
Qy 501 TrpLysAsnLysGluGlnHisLeuSerGluAsnGluProValAspThrAsnSerAspAsn 520  
Db 1526 TGGAAAAATAGGAGCAGCATCTATCTGAGAAATGAGCCTGTGGACACAACTCAGACAAT 1585  
Qy 521 AsnLeuPheThrAspThrAspLeuLysSerIleValLysAsnSerAlaSerLysSerHis 540  
Db 1586 AACCTATTATTCAGATACAGATTTAAATCTATTCTGAAAAATTTCTGCCAGTAAATCTCAT 1645  
Qy 541 AlaAlaGluLysLeuArgSerAsnLysLysArgGluMetAspAspValAlaIleGluAsp 560  
Db 1646 GCTCAGAAAAGCTTAAGATCAATATAAAAAGGAGAAATGATGATGTGGCCATAGAAAT 1705  
Qy 561 GluValLeuGluGlnLeuPheLysAspThrLysProGluLeuGluIleAspValLysVal 580  
Db 1706 GAAGTATTGGAAACAGTTATTTCAGAGACACAAAACAGAGTTAGAAAATTTGATGTGAAAGTT 1765  
Qy 581 GlnLysGlnGluLysAspValAsnValArgLysArgProArgMetAspIleGluThrAsn 600  
Db 1766 CAAAACAGGAGGAGAGATGTCAATGTTAGAAAAAGGCCAAGGATGAGATATAGAAACAAAT 1825  
Qy 601 AspThrPheSerAspGluAlaValProGluSerSerLysIleSerGlnGluAsnGluIle 620  
Db 1826 GACACTTTTCACTGATGAGCAGTACCAAGAGTAGCAAAATATCTCAAGAAAATGAAATTT 1885  
Qy 621 GlyLysLysArgGluLeuLysGluAspSerLeuTrpSerAlaLysGluIleSerAsnAsn 640  
Db 1886 GGGAGAGAAACGTGAACCTCAAGGAGAGCTCATATGTTGTTGAGTAAAGAAAATATCTAACAA 1945  
Qy 641 AspLysLeuGlnAspAspSerGluMetLeuProLysLysLeuLeuLeuThrGluPheArg 660  
Db 1946 GACAAACTTCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2005  
Qy 661 SerLeuValLysLysAsnSerThrSerArgAsnProSerGlyIleAsnAspAspTrpGly 680  
Db 2006 TCACTGTGTATTAATAACTCTACTTCCAGAAAATCCATCTGTCATTAATGATGATGATGAT 2065  
Qy 681 GlnLeuLysAsnPheLysLysPheLysLysValThrTrpProGlyAlaGlyLysLeuPro 700  
Db 2066 CAATATAAAATTTCAAGAAAATTCAAAAGAGGTACATATCTCTGAGCAGGAGAAAATCTCCA 2125  
Qy 701 HistIleGlyGlySerAspLeuIleAlaHisIleAlaArgLysAsnThrGluLeuGlu 720  
Db 2126 CACATCATTCAGAGATCAGATCTAATAGCTCATCATGCTCGAAAGAAATACAGAACTAGA 2185  
Qy 721 GluTrpLeuArgGlnGluMetGluValGlnAsnGlnHisAlaLysGluGluSerLeuAla 740  
Db 2186 GAGTGGCTAAGGAGGAGAAATGGAGGTACAAAATTCACATTCACAAAAGAGAGAGTCTCTTCT 2245

**THIS PAGE BLANK (USPTO)**

BEST AVAILABLE COPY

Qy 741 AspAspLeuPheArgTyrAsnProTyrLeuLysArgArg 754  
 Db 2246 GATGATCTTTTACATCAATCTTATTTAAAGAGAGA 2287

RESULT 2

US-08-938-105-2  
 ; Sequence 2, Application US/08938105  
 ; Patent No. 6353151  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Leinwand, Leslie A.  
 ; APPLICANT: Vikstrom, Karen L.  
 ; TITLE OF INVENTION: TRANSGENIC MODEL FOR HEART FAILURE  
 ; NUMBER OF SEQUENCES: 3  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Sheridan Ross P.C.  
 ; STREET: 1700 Lincoln St., Suite 3500  
 ; CITY: Denver  
 ; STATE: CO  
 ; COUNTRY: U.S.A.  
 ; ZIP: 80203  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/938,105  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Crook, Wamell M.  
 ; REGISTRATION NUMBER: 31,071  
 ; REFERENCE/DOCKET NUMBER: 3595-4  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (303) 863-9700  
 ; TELEFAX: (303) 863-0223  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5661 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: CDNA  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 1..5661  
 ; US-08-938-105-2

Alignment Scores:  
 Pred. No.: 4.76e-08 Length: 5661  
 Score: 175.00 Matches: 102  
 Percent Similarity: 37.98% Conservative: 67  
 Best Local Similarity: 22.92% Mismatches: 141  
 Query Match: 4.49% Indels: 135  
 DB: 4 Gaps: 19

US-09-837-602-2 (1-754) x US-08-938-105-2 (1-5661)

Qy 326 GlnGlyHisProSerThrGlyLeuLysThrThrThrProGlyProSerLeuSerGlnGly 345  
 Db 2268 CAGGACGCCCTGCTCT--GGTTATCCAGTGGAAATCCCGCCCTTCATGGGGTCAAGAA 2324  
 Qy 346 ValSerValAspGluLysLeuMetProSer-AlaProValAsnThrThrThrThrValAl 365  
 Db 2325 TTGGCCGTGGTGAAGTCTACTTCAGATCAACGCCGCTGCTGAAGAGC-----GC 2375  
 Qy 365 AspThrGluSerGluGlnAlaAspThrTrpAspLeuSerGluArgProLys----- 382  
 Db 2376 AGACACAGAGAAGAGAGATGGCCAAATGAAAGAGAGTTCCGGCGAGTCAAAGATGCAC 2435  
 Qy 383 -----GluLeuLysValSerLysMetGluGlnLysPheArgMetLysGlnAs 399  
 Db 2436 AGAGAAGTCTGAGGCTCGCCGCAAGAGAGCTGGAGAGAGATGGTGTCTCTGCTGCAGGA 2495

Qy 399 pAlaProThrValLysGluSerCysLysThrSerSerAsnAsnAsnSerMetValSerAs 419  
 Db 2496 GAAGAATGACCTGCAGCTCCAAGTCGAGCGGCAACAGCAAC----- 2538  
 Qy 419 nThrLeuAlaLysMetArgIleProAsnTyrGlnLeuSerProThrLysLeuProSerIl 439  
 Db 2539 -----CT 2540  
 Qy 439 eAsnLysSerLysAspArgAlaSerGlnGlnGlnGlnThrAsnSerIleArgAsnTyrPh 459  
 Db 2541 GGCAGATGCCGAGGCGCTGCAGCAG-----CTGATCAAGAACAGAT 2585  
 Qy 459 eGlnProSerThrLysLysArg-----GluArgAspGluGluAsnGlnLysMetSe 476  
 Db 2586 CCAGCTGGAGGCCAAGGTGAAGAGATGACCGAGGCTGGAGGACGAGGAGATGAA 2645  
 Qy 476 r-----SerCysLysSerAlaArgIleGluThrSerCysSer---LeuLeuGluGl 492  
 Db 2646 CGCCGAGCTCACCGGCCAAGAGCGCAAGCTGGAAGACGAGTGTCTCAGAGCTCAAGAAAGA 2705  
 Qy 492 nThrGlnProAlaThrProSerLeuTrpLys---AsnLysGluGlnHisLeuSerGluAs 511  
 Db 2706 TATCGATGACCTGGAGCTGACCTGCGCAAGTGGAGAGGAAAGAACGCAACAGAGAA 2765  
 Qy 511 nGluProValAspThrAsnSerAspAsnAsnLeuPheThrAspThrAspLeuLysSerIl 531  
 Db 2766 CAAG-----GTTAAACCT 2780  
 Qy 531 eValLysAsnSerAlaSerLysSerHisAlaAlaGluLysLeuArgSerAsnLysLys-- 550  
 Db 2781 GACAGAGAGATGGCGCGCTGCAGCAGATCATTTGCCAAGCTGACCAAGGAGAGAAAGC 2840  
 Qy 551 -----ArgGluMetAspAspValAlaIleGluAspGluValLeuGl 564  
 Db 2841 TCTTCAAGAGGCCACCAGCAAGCCCTAGTACCTTCAGGCTGAGGAGAGAAAGTCAA 2900  
 Qy 564 uGlnLeuPheLysAspThrLysProGluLeuGluIleAspValLysValGlnLysGlnGl 584  
 Db 2901 CACACTG-----ACCAAGTCTAAAGTCAAGCTGGAGCAGCAGCTGGATCTGGA 2951  
 Qy 584 uGluAspValAsnValArgLysArgProArgMetAspIleGluThrAsnAspThrPheSe 604  
 Db 2952 GGGATCCTCGAGCAGGAGAGAGGTGGCATCTGACCTGGAGCGCA----- 2997  
 Qy 604 rAspGluAlaValProGluSerSerLysLysIleSerGlnGluAsnGluIleGlyLysLysAr 624  
 Db 2998 -----GCAAGCG 3005  
 Qy 624 gGluLeuLysGluAspSerLeuTrpSerAlaLysGluLysSerAsn-----AsnAspLy 642  
 Db 3006 GAAGCTGGAGGGTGACCTGACCTGACCCAGGAGAGCATCATCGACCTGGAGNACGACAA 3065  
 Qy 642 sLeuGlnAspAspSerGluMetLeuProLysLysLeuLeuThrGluPheArgSerLe 662  
 Db 3066 GCTTCAG-----CTGGAGGAAAGCTCAAGAGAAAGAGTT----- 3102  
 Qy 662 uValLysAsnSerThrSerArgAsnProSerGlyIleAsnAspAspTyrGly---Gl 681  
 Db 3103 -----GACATCAGTCAGCAGAACAGATAAATAGAGAGCAGCAGGCCCTGGC 3149  
 Qy 681 nLeuLysAsnPheLysPheLysValThrTyrProGlyAlaGlyLysLeuProHi 701  
 Db 3150 CCTTCAGCTGCAGAAACTGAGAA----- 3177  
 Qy 701 sIleIleGlyGlySerAspLeuIleAlaHisAlaArgLysAsnThrGluLeuGluGl 721  
 Db 3178 -----AACCAAGGCGCAGCATCGAGGAGCTGAGGA 3206  
 Qy 721 uTrpLeuArgGlnGluMetGluValGlnAsnGlnHisAlaLysGluGluSerLeuAlaAs 741  
 Db 3207 GGAGCTAGAGCGGAG-----GCCACAGCCCGGCCCAAGGTGGAGAGCTGCGCTC 3257

**THIS PAGE BLANK (USP10)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 6, 2004, 10:40:04 ; Search time 127 Seconds  
(without alignments)

2620.495 Million cell updates/sec

Title: us-09-837-602-2

Perfect score: 3899

Sequence: 1 MWKLLPAGGAGGEPYRLLT.....KESSLADLFRNPKRRR 754

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-O=/cg2\_1/USPTO\_spool/US09837602/runat 06012004 103959 12455/app\_query.fasta\_1.903  
-DB=Issued\_Patents\_NA -QWTS=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09837602 @CGN 1.1 56 @runat 06012004 103959 12455 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:

- 1: /cg2\_6/ptodata/1/ina/5A.COMB.seq:\*
- 2: /cg2\_6/ptodata/1/ina/5B.COMB.seq:\*
- 3: /cg2\_6/ptodata/1/ina/6A.COMB.seq:\*
- 4: /cg2\_6/ptodata/1/ina/6B.COMB.seq:\*
- 5: /cg2\_6/ptodata/1/ina/6C.COMB.seq:\*
- 6: /cg2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3896	99.9	4386	US-09-300-008B-1	Sequence 1, Appli
2	175	4.5	5661	US-08-938-105-2	Sequence 2, Appli
3	169	4.3	3384	US-08-923-992A-5	Sequence 5, Appli
4	166	4.3	8503	US-09-620-312D-130	Sequence 130, App
5	164.5	4.2	8948	US-09-643-537-119	Sequence 119, App
6	164.5	4.2	8948	US-09-480-884A-119	Sequence 119, App
7	164.5	4.2	8948	US-09-542-615A-119	Sequence 119, App
8	164.5	4.2	8948	US-09-606-421B-119	Sequence 119, App
9	163	4.2	8257	US-09-595-684B-30	Sequence 30, Appli
10	162.5	4.2	5857	US-09-220-132-79	Sequence 79, Appli
11	162	4.2	3135	US-09-107-532A-1575	Sequence 1575, Ap
12	161	4.1	3294	US-08-923-992A-7	Sequence 7, Appli

13	157.5	4.0	2672	3	US-09-214-564A-5	Sequence 5, Appli
14	157.5	4.0	2815	3	US-09-214-564A-1	Sequence 1, Appli
15	157	4.0	4200	1	US-08-242-932-1	Sequence 1, Appli
16	157	4.0	4200	1	US-08-714-481-1	Sequence 1, Appli
17	157	4.0	4200	3	US-08-923-992A-1	Sequence 1, Appli
18	157	4.0	4200	5	PCT-US95-08111-1	Sequence 1, Appli
19	156.5	4.0	3393	3	US-09-104-324B-1	Sequence 1, Appli
20	156.5	4.0	3393	3	US-09-162-713-1	Sequence 1, Appli
21	156	4.0	3492	3	US-08-923-992A-9	Sequence 9, Appli
22	155.5	4.0	1704	2	US-08-630-822A-67	Sequence 67, Appli
23	155.5	4.0	1704	2	US-09-005-069-67	Sequence 67, Appli
24	155.5	4.0	1704	4	US-09-171-156A-26	Sequence 26, Appli
25	155.5	4.0	1704	4	US-09-004-730A-26	Sequence 26, Appli
26	155.5	4.0	1704	4	US-08-981-799A-26	Sequence 26, Appli
27	155	4.0	30549	4	US-09-134-001C-322	Sequence 322, App
28	154.5	4.0	6755	3	US-08-931-999-4	Sequence 4, Appli
29	151	3.9	1830121	4	US-09-557-884-1	Sequence 1, Appli
30	151	3.9	1830121	4	US-09-643-990A-1	Sequence 1, Appli
31	150.5	3.9	3063	4	US-08-294-312B-3	Sequence 3, Appli
32	150.5	3.9	3063	4	US-08-468-024B-3	Sequence 3, Appli
33	150.5	3.9	3063	4	US-09-708-200-12	Sequence 12, Appli
34	150.5	3.9	5194	1	US-09-599-652-1	Sequence 1, Appli
35	150.5	3.9	5194	2	US-08-642-846-1	Sequence 1, Appli
36	150.5	3.9	5194	4	US-09-284-604-1	Sequence 1, Appli
37	150	3.8	1383	2	US-08-630-822A-82	Sequence 82, Appli
38	150	3.8	1383	2	US-09-005-069-82	Sequence 28, Appli
39	150	3.8	1383	4	US-09-171-156A-28	Sequence 28, Appli
40	150	3.8	1383	4	US-09-004-730A-28	Sequence 28, Appli
41	150	3.8	1383	4	US-08-981-799A-28	Sequence 28, Appli
42	149.5	3.8	2617	1	US-08-430-024-1	Sequence 1, Appli
43	149.5	3.8	2617	1	US-08-782-009-1	Sequence 1, Appli
44	149.5	3.8	2617	3	US-09-017-302-1	Sequence 1, Appli
45	147.5	3.8	3730	1	US-08-242-932-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-09-300-008B-1

- ; Sequence 1, Application US/09300008B
- ; Patent No. 6458534
- ; GENERAL INFORMATION:
- ; APPLICANT: Concannon et al.
- ; TITLE OF INVENTION: A GENE ASSOCIATED WITH NIJMEGEN BREAKAGE SYNDROME, ITS GENE PRODUCT AND METHODS FOR THEIR USE
- ; FILE REFERENCE: 9924-0003-228
- ; CURRENT APPLICATION NUMBER: US/09/300,008B
- ; CURRENT FILING DATE: 1999-04-27
- ; PRIOR APPLICATION NUMBER: US 60/083,269
- ; PRIOR FILING DATE: 1998-04-27
- ; NUMBER OF SEQ ID NOS: 64
- ; SOFTWARE: FastSeq for Windows Version 3.0
- ; SEQ ID NO 1
- ; LENGTH: 4386
- ; TYPE: DNA
- ; ORGANISM: Homo sapien
- ; FEATURE:
- ; NAME/KEY: CDS
- ; LOCATION: (26)...(2287)
- ; US-09-300-008B-1

Alignment Scores:

Pred. No.: 0  
Score: 3896.00  
Percent Similarity: 100.00%  
Best Local Similarity: 99.87%  
Query Match: 99.92%  
DB: 4  
Length: 4386  
Matches: 753  
Conservative: 1  
Mismatches: 0  
Indels: 0  
Gaps: 0

US-09-837-602-2 (1-754) x US-09-300-008B-1 (1-4386)

Oy 1 MetTrpysLeuLeuProAlaAlaGlyProAlaGlyGluProtyrArgLeuLeuThr 20  
|||||

## BEST AVAILABLE COPY

Db	26	ATGTGGAAAC	TGCTGCCGCCGCCGGGCCCGCAGAGAGAAACATACAGACTTTTGACT	85
Qy	21	GlyValGluTyrValValGlyArgLysAsnCysAlaIleLeuIleGluAsnAspGlnSer	40	
Db	86	GGCGTTGAGTACGTTGTTGGAAGGAAACCTGTGCCATTCTGATTTGAATGATCAGTCG	145	
Qy	41	IleSerArgAsnHisAlaValLeuThrAlaAsnPheSerValThrAsnLeuSerGlnThr	60	
Db	146	ATCAGCGGAAATCATGCTGTGTTAACTGCTAACTTTTCTGTGTAAACCAACTGAGTCAACA	205	
Qy	61	AspGluIleProValLeuThrLeuLysAsnAspAsnSerLysTyrGlyThrPheValAsnGlu	80	
Db	206	GATGAATCCCTGTATTGACATTAAAGATAAATCTAAGTATAGTACTTTGTTTAAATGAG	265	
Qy	81	GluLysMetGlnAsnGlyPheSerArgThrLeuLysSerGlyAspGlyIleThrPheGly	100	
Db	266	GAAAAATGCAGATGGCTTTTCCGAACTTTGAAGTCGGGGATGGTATTACTTTTGGGA	325	
Qy	101	ValPheGlySerLysPheArgIleGluTyrGluProLeuValAlaCysSerSerCysLeu	120	
Db	326	GTGTTTGGAGTAAATTCAGAAATAGAGTATGAGCCTTTGGTGTGCATGCTCTCTTGTGTTA	385	
Qy	121	AspValSerGlyLysThrAlaLeuAsnGlnAlaIleLeuGlnLeuGlyGlyPheThrVal	140	
Db	386	GATGTCCTCGGAAAACTGCTTTTAAATCAAGCTATATTGCAACTTGGAGGATTTTACTGTA	445	
Qy	141	AsnAsnTrpThrGluGluCysThrHisLeuValMetValSerValLysValThrIleLys	160	
Db	446	AACAATTTGGACAGAAGAATGCACCTCTGTCTATGGTATCAGTGAAGTTACCATTTAA	505	
Qy	161	ThrIleCysAlaLeuIleCysGlyArgProIleValLysProGluTyrPheThrGluPhe	180	
Db	506	ACAATATGTGCACTCATTTGTGGACGTCCTCAATTTGTAAGCCAGAAATATTTTACTGAATTC	565	
Qy	181	LeuLysAlaValGlnSerLysLysGlnProProGlnIleGluSerPheTyrProProLeu	200	
Db	566	CTGAAGACAGTTGAGTCCAGAAACAGCAGCTCCACAAATTGAAAGTTTTTATCCCACTCTT	625	
Qy	201	AspGluProSerIleGlySerLysAsnValAspLeuSerGlyArgGlnGluArgLysGln	220	
Db	626	GATGAAACCACTATTGGAGTAAAAATGTTGATCTGCAGACCGCAGAGAAAGAAACAA	685	
Qy	221	IlePheLysGlyLysThrPheIlePheLeuAsnAlaLysGlnHisLysLysLeuSerSer	240	
Db	686	ATCTTCAAGGGAAAAACATTTATATTTTGAATSCCAACAGCATAAGAAATTCAGTTCC	745	
Qy	241	AlaValValPheGlyGlyGlyLysAlaArgLeuIleThrGluGluAsnGluGluHis	260	
Db	746	GCAGTTGCTCTTTGGAGGTGGGGAAGCTAGGTTGTATAACAGAAGAGAAATGAAGAGAACAT	805	
Qy	261	AsnPhePheLeuAlaProGlyThrCysValValAspThrGlyIleThrAsnSerGlnThr	280	
Db	806	AAITTCITTTTGGCTCCGGNAACGTGTGTTGATACAGAAATAACAACTTCACAGACC	865	
Qy	281	LeuIleProAspCysGlnLysLysTrpIleGlnSerIleMetAspMetLeuGlnArgGln	300	
Db	866	TTAATTCCTGACTCTCAGAGAAATGGATTCACTCAATATGGATATGCTCCCAAGGCAA	925	
Qy	301	GlyLeuArgProIleProGluAlaGluIleGlyLeuAlaValIlePheMetThrThrLys	320	
Db	926	GGTCTTAGACCTATTCTCCTGAAGCAGAAATTTGGAATGGCGGTGATTTTTCATGACTACAAAG	985	
Qy	321	AsnTyrCysAspProGlnGlyHisProSerThrGlyLysThrThrThrProGlyPro	340	
Db	986	AATTACTGTGATCTCTCAGGGCCATCCCAAGTACAGGATTTAAAGACAAACAACCTCCAGGACCA	1045	
Qy	341	SerLeuSerGlnGlyValSerValAspGluLysLeuMetProSerAlaProValAsnThr	360	
Db	1046	AGCCTTTCACAGGCGTGTGATGTATGAAAAAATAATATGTCACAGCGCCCCAGTGAAACACT	1105	
Qy	361	ThrThrTyrValAlaAspThrGluSerGluGlnAlaAspThrTrpAspLeuSerGluArg	380	
Db	1106	ACAACTACGTAGCTGACAGAAATCAGACAGCAGATCATCGGATTTGAGTGAAGG	1165	

Qy	381	ProLysGluIleLysValSerLysMetGluGlnLysPheArgMetLeuSerGlnAspAla	400
Db	1166	CCAAAAGAAATCAAAGTCTCAAAATATGGAAACAAAAATTCAGAAATGCTTTTCAACAAGATGCA	1225
Qy	401	ProThrValLysGluSerCysLysThrSerSerAsnAsnAsnSerMetValSerAsnThr	420
Db	1226	CCCACTGTAAGAGAGCTCTGCAAAACAAGCTCTAATAATAAGTAGTAGTATGCTCAAAATACT	1285
Qy	421	LeuAlaLysMetArgIleProAsnTyrGlnLeuSerProThrLysLeuProSerIleAsn	440
Db	1286	TTGGCTAAGATGAGAATCCCAAACTATCAGCTTTCCACCAACTAAATTTGCCAGTATAAAT	1345
Qy	441	LysSerLysAspArgAlaSerGlnGlnGlnGlnThrAsnSerIleArgAsnTyrPheGln	460
Db	1346	AAAAGTAAAGATAGGGCTTCTCAGCAGCAGCAGCAACCTCCATCAGAACAACCTACTTTCAG	1405
Qy	461	ProSerThrLysLysArgGluArgAspGluGluAsnGlnGluMetSerSerCysLysSer	480
Db	1406	CCGCTACCAAAAAGGGGAAGGGATGAAGAAATCAAGAAATGCTTCATGCAAAATCA	1465
Qy	481	AlaArgIleGluThrSerCysSerLeuLeuGluGlnThrGlnProAlaThrProSerLeu	500
Db	1466	GCAAGATAGAAACGCTGTGTTCTCTCTTTAGAACAAACACACCTGCTACACCTCATTTG	1525
Qy	501	TrpLysAsnLysGluGlnHisLeuSerGluAsnGluProValAspThrAsnSerAspAsn	520
Db	1526	TGGAAATAAAGAGCAGCATCTATCTGAGAATGAGCCTGTGGACACAAACTCAGACAAT	1585
Qy	521	AsnLeuPheThrAspThrAspLeuLysSerIleValLysAsnSerAlaSerLysSerHis	540
Db	1586	AACCTATTTACAGATACAGATTTAAAAATCTATTGTGAAAAATTCGCCAGTAAATCTCAT	1645
Qy	541	AlaAlaGluLysLeuArgSerAsnLysLysArgGluMetAspAspValAlaIleGluAsp	560
Db	1646	GCTGCGAAAAGCTAAGATCAATAAAAAAGGGAAATGGATGATGTGCCCATAGAAAGAT	1705
Qy	561	GluValLeuGluGlnLeuPheLysAspThrLysProGluLeuGluIleAspValLysVal	580
Db	1706	GAAGTATTGGAACAGTTATTCAAGGACACAAAACCCAGAGTTAGAAATTCGATGTGAAGT	1765
Qy	581	GlnLysGlnGluGluAspValAsnValArgLysArgProArgMetAspIleGluThrAsn	600
Db	1766	CAAAAAACAGAGAAAGATGTCAATGTGTAGAAAAGGCCAAGATGATATAGAAAACAAAT	1825
Qy	601	AspThrPheSerAspGluAlaValProGluSerSerLysIleSerGlnGluAsnGluIle	620
Db	1826	GACACTTTCAGTGTGAGCGAGTACCAGAAAGTAGCAAAATATCTCAGAAATGAAATTT	1885
Qy	621	GlyLysLysArgGluLeuLysGluAspSerLeuTrpSerAlaLysGluIleSerAsnAsn	640
Db	1886	GGGAAGAAACGCTGAACCTCAAGGAAGACTCACTATGTGTAGCTAAAGAAATATCTTAACAAT	1945
Qy	641	AspLysLeuGlnAspAspSerGluMetLeuProLysLysLeuLeuLeuThrGluPheArg	660
Db	1946	GACAAACTTCAGATGATAGTAGAGTCTTCCAAAAAAGCTGTATTGTGCTGAATTTTGA	2005
Qy	661	SerLeuValIleLysAsnSerThrSerArgAsnProSerGlyIleAsnAspAspTyrGly	680
Db	2006	TCACTGGTGATTAAAAACCTACTTCCAGNAATCCATCTGGCAATAATGATGNTATGGT	2065
Qy	681	GlnLeuLysAsnPheLysLysPheLysLysValThrTyrProGlyAlaGlyLysLeuPro	700
Db	2066	CAACTAAAAAATTTCAAGAAATTCAAAAAGGTCACATATCTCTGGACAGAGAAACCTCCA	2125
Qy	701	HisIleIleGlyLysSerAspLeuIleAlaHisHisAlaArgLysAsnThrGluLeuGlu	720
Db	2126	CACATCATTTGGAGGATCAGATCTTAATAGTCTCATGTGCTCGAAAGAANTACAGAACTAGAA	2185
Qy	721	GluTrpLeuArgGlnGluMetGluValGlnAsnGlnHisAlaLysGluGluSerLeuAla	740
Db	2186	GAGTGGCTAAGCAGAAATGAGAGTACAAATCAACATGCAAAAGAAAGTCTCTTGCT	2245

BEST AVAILABLE COPY

Qy 741 AspAspLeuPheArgTyrAsnProTyrLeuLysArgArg 754  
 Db 2246 GATGATCTTTTATAGATCAATCTCTTATTTAAAGGAGAAGA 2287

## RESULT 2

US-08-938-105-2  
 ; Sequence 2, Application US/08938105  
 ; Patent No. 6353151  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Leinwand, Leslie A.  
 ; APPLICANT: Vikstrom, Karen L.  
 ; TITLE OF INVENTION: TRANSGENIC MODEL FOR HEART FAILURE  
 ; NUMBER OF SEQUENCES: 3  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Sheridan Ross P.C.  
 ; STREET: 1700 Lincoln St., Suite 3500  
 ; CITY: Denver  
 ; STATE: CO  
 ; COUNTRY: U.S.A.  
 ; ZIP: 80203  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; FILING DATE: US/08/938.105  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Crook, Wanneil M.  
 ; REGISTRATION NUMBER: 31,071  
 ; REFERENCE/DOCKET NUMBER: 3595-4  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (303) 863-9700  
 ; TELEFAX: (303) 863-0223  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5661 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 1..5661  
 ; US-08-938-105-2

Alignment Scores:  
 Pred. No.: 4.76e-08 Length: 5661  
 Score: 175.00 Matches: 102  
 Percent Similarity: 37.98% Conservative: 67  
 Best Local Similarity: 22.92% Mismatches: 141  
 Query Match: 4.49% Indels: 135  
 DB: 4 Gaps: 19

US-09-837-602-2 (1-754) x US-08-938-105-2 (1-5661)

Qy 326 GlnGlyHisProSerThrGlyLeuLysThrThrThrProGlyProSerLeuSerGlnGly 345  
 Db 2268 CAGGAGCGCCCTGCT---GGTTATCCAGTGGAAACATCCGCGCTTCATGGGGGTCAAGAA 2324  
 Qy 346 ValSerValAspGluLysLeuMetProSer-AlaProValAsnThrThrThrValAl 365  
 Db 2325 TTGGCCGTGGATGAAGCTCTACTCAAGATCAAGCCGCTGCTGAAGAGC-----GC 2375  
 Qy 365 aAspThrGluSerGlnGlnAlaAspThrTrpAspLeuSerGluArgProLys----- 382  
 Db 2376 AGACACAGAGAAGGAGATGGCCACATGAAGAGAGAGTTCCGGCGAGTCAAGATGCAC 2435  
 Qy 383 -----GluLeuLysValSerLysMetGluGlnLysPheArgMetLeuSerGlnAs 399  
 Db 2436 AGAGAAGTCTGAGGCTCGCCCGCAAGGAGCTGGAGGAGAAGATGGTGTCTCTGTCAGGA 2495

Qy 399 pAlaProThrValLysGluSerCysLysThrSerSerAsnAsnSerMetValSerAs 419  
 Db 2496 GAAGAATGACCTGCAGCTCCAAGTCGAGCGGCAACAAGACAAC----- 2538  
 Qy 419 nThrLeuAlaLysMetArgIleProAsnTyrGlnLeuSerProThrLysLeuProSerIl 439  
 Db 2539 -----CT 2540  
 Qy 439 eAsnLysSerLysAspArgAlaSerGlnGlnGlnInThrAsnSerIleArgAsnTyrPh 459  
 Db 2541 GGCAGATGCCGAGGAGCGCTGCCACCAG-----CTGATCAAGAACACAGAT 2585  
 Qy 459 eGlnProSerThrLysLysArg-----GluArgAspGluGlnAsnGlnGluMetSe 476  
 Db 2586 CCAGCTGGAGGCCAAGGTGAAGGAGATACCGAGAGAGCTCGAGGACGAGGAGGATGAA 2645  
 Qy 476 r-----SerCysLysSerAlaArgIleGluThrSerCysSer---LeuLeuGluGl 492  
 Db 2646 CGCCGAGCTCACGCCCAAGAGCGCAAGCTGGAGAGAGAGTGTCTCAGAGCTCAAGAAGA 2705  
 Qy 492 nThrGlnProAlaThrProSerLeuTyrLys---AsnLysGluGlnHisLeuSerGluAs 511  
 Db 2706 TATCGATGACCTGGAGCTGACCTGCCCAAGGTGGAGAGAGAGAACGACCGACACAGAGA 2755  
 Qy 511 nGluProValAspThrAsnSerAspAsnLeuPheThrAspThrAspLeuLysSerIl 531  
 Db 2766 CAAG-----GTTAAACCT 2780  
 Qy 531 eValLysAsnSerAlaSerLysSerHisAlaAlaGluLysLeuArgSerAsnLysLys-- 550  
 Db 2781 GACAGAGGAGATGCCCGGCTGGACGAGATCATTTGCCAAGCTGACCAAGGAGAGAAAGC 2840  
 Qy 551 -----ArgGluMetAspAspValAlaIleGluAspGluValLeuGl 564  
 Db 2841 TCTTCAAGAGGCCACCAGCAAGCCCTAGATGACCTTCAGGCTGAGGAGAACAGAGTCAA 2900  
 Qy 564 uGlnLeuPheLysAspThrLysProGluLeuGluIleAspValLysValGlnLysGlnGl 584  
 Db 2901 CACACTG-----ACCAAGTCTAAAGTCAAGCTGGAGCAGCAGCTGGATGATCGGA 2951  
 Qy 584 uGluAspValAsnValArgLysArgProArgMetAspIleGluThrAsnAspThrPheSe 604  
 Db 2952 GGGATCCCTGGAGCAGGAGAAGAGTGCATGGACCTGGAGCGA----- 2997  
 Qy 604 rAspGluAlaValProGluSerSerLysIleSerGlnGluAsnGluIleGlyLysLysAr 624  
 Db 2998 -----GCAAGCG 3005  
 Qy 624 gGluLeuLysGluAspSerLeuTrpSerAlaLysGluIleSerAsn-----AsnAspLy 642  
 Db 3006 GAAGCTGGAGGGTGACCTGAAGCTGACCCAGGAGAGCATCATGACCTGGAGAACGACAA 3065  
 Qy 642 sLeuGlnAspAspSerGluMetLeuProLysLysLysLeuLeuLeuThrGluPheArgSerLe 662  
 Db 3066 GCTTCAG-----CTGGAGGAAAAAGCTCAAGAAGAAAGAGTTT----- 3102  
 Qy 662 uValIleLysAsnSerThrSerArgAsnProSerGlyIleAsnAspAspTyrGly---G1 681  
 Db 3103 -----GACATCAGTCAGCAAGACAGTAAATAAGAGCAGCAGGAGCCCTGGC 3149  
 Qy 681 nLeuLysAsnPheLysLysPheLysLysValThrThrProGlyAlaGlyLysLeuProH1 701  
 Db 3150 CCTTCAGCTCAGAGAACTGAAGGA----- 3177  
 Qy 701 sIleIleGlyGlySerAspLeuIleAlaHisHisAlaArgLysAsnThrGluLeuGluGl 721  
 Db 3178 -----AACCAGGCGCAGCATCGAGGAGCTGGAGGA 3206  
 Qy 721 uTrpLeuArgGlnGluMetGluValGlnAsnGlnHisAlaArgLysGluGluSerLeuAlaAs 741  
 Db 3207 GGAGCTAGAGCGGAG-----CGCAGCGCCCGGCAAGGTGGAGAGCTGCGCTC 3257

BEST AVAILABLE COPY

QY 741 pAspLeuPheArg 745  
Db 3258 AGACCTGACCGG 3270

RESULT 3  
US-08-923-992A-5  
; Sequence 5, Application US/08923992A  
; Patent No. 6280738  
; GENERAL INFORMATION:  
; APPLICANT: Tai, Joseph Y.  
; APPLICANT: Blake, Milan S.  
; TITLE OF INVENTION: No. 6280738-IgA Fc Binding Forms of the Group B  
; TITLE OF INVENTION: Streptococcal Beta Antigens  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/923.992A  
; FILING DATE: 05-SEP-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/024,707.  
; FILING DATE: 06-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1438.0140001/RWE  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3384 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..3384  
US-08-923-992A-5

Alignment Scores:  
Pred. No.: 8.99e-08 Length: 3384  
Score: 169.00 Matches: 142  
Percent Similarity: 37.45% Conservative: 125  
Best Local Similarity: 19.92% Mismatches: 238  
Query Match: 4.33% Indels: 208  
DB: 3 Gaps: 38

US-09-837-602-2 (1-754) x US-08-923-992A-5 (1-3384)

QY 192 GlnIleGluSerPheTyrProProLeuAspGluProSerIleGlySerLysAsnValAsp 211  
Db 283 CAGAAAAATGAGTTTAAACAAATAATGATGAAACAAATGATTCGATGCAATTATTAGAA 342

QY 212 LeuSerGlyArg  
Db 343 TTGAAATCAATTTACGAACTAATAGACTGTACACATCAACAAATGAGAGATT 402

QY 222 PheLysGlyLysThrPheIlePheLeuAsnAlaLysGlnHisLysLysLeuSerSerAla 241  
Db 403 GAGAAAGATAAG-----AAAGCTAAGCAACAGAAATCTCTGAAACAGTCA 447

QY 242 ValValPheGlyGlyGluAlaArgLeuIleThrGluAsnGluGluHisAsn 261  
Db 448 -----GATACAAAGTAGACTAGCAATATTGCAAGAGAGCTTTAAT 489

QY 262 PhePheLeuAlaProGlyThrCysValValAsp---ThrGlyIleThrAsnSerGlnThr 280  
Db 490 CATCAAAAAAGTCCAGTTGAAAAAATGCGACGCCAAAGGGAATCACAATGAAGAT--- 546

QY 281 LeuIleProAspCysGlnLysLysTyrPilleGlnSerIleMetAspMetLeuGlnArgGln 300  
Db 547 -----AAAGATTCTATGCTGAAAAAATCGAAGATATTCGTAAACAAGCTCAACAAGCA 600

QY 301 GlyLeuArgProIleProGluAlaGluIle-----GlyLeuAlaValIlePheMetThr 318  
Db 601 GATAAAAAAGCAAGATCCGGAAGTAAAGGTTCTGTAAGAACTAGGTAAACTCTTTAGTTCA 660

QY 319 ThrLysAsnTyrCysAspProGlnGlyHisProSerThrGlyLeuLysThrThrPro 338  
Db 661 ACTAAAGCTGGTCTGGATCAAGAAATTCATGACATGTGAAGAAAGAACGAGT----- 714

QY 339 GlyProSerLeuSerGlnGlyValSerValAspGluLysLeuMetProSerAlaProVal 358  
Db 715 -----AGTGAGGAAATATCTCAGAAAGTTGATGAACACTAT-----GCT 753

QY 359 AsnThrThrTyrValAlaAspThrGluSerGluGlnAlaAspThrTyrAspLeuSer 378  
Db 754 AATAGCTTCAGAACCTTCTCTGAAAGAACTAGTAAAGCAAGCAATACCAAT 813

QY 379 GluArgProLysGluIleLysValSerLysMetGlu-----GlnLys----- 392  
Db 814 GAAACAAGCTACACAAGTTAAATAATCAATTTAGAAAACGCTCAAAAGCTCAAGAAATG 873

QY 393 -----PheArgMetLeuSerGlnAspAlaPro 401  
Db 874 CAACCTCTTATCAAGAAACGAATGTGAATTTGTAAGGCTATGATGAGAGCTTTGGAG 933

QY 402 ThrValLysGluSerCysLysThrSerSerAsnAsn-----SerMetValSerAsn 419  
Db 934 CAGGTTGAGAGGAATTAACAATAATTCGGAAGCTAATTAGAACATTTGGTTGGCAA 993

QY 420 ThrLeuAlaLysMetArgIleProAsnTyrGlnLeuSerProThrLys---LeuProSer 438  
Db 994 TCTAAAGAAATCGTAAGAGAATACGAAGGAAATCTTAATCAATCTTAAATCTTCCAGAA 1053

QY 439 IleAsnLysSerLysAspArgAlaSerGln-----GlnGlnGlnThrAsnSerIleArg 456  
Db 1054 TTAAGCAACTAGAGAGGAGCTCATTGAAAGTTGAAACAAAGTTGTGAGGATTTTGA 1113

QY 457 AsnTyrPhe-----GlnProSerThrLysLysArg---GluArgAsp----- 469  
Db 1114 AAAAAATTTAAACGTCAGAGCAAGTCACACCAAAAAACGTCGCAACGAGATTTAGCT 1173

QY 470 -----GluGluAsnGlnGluMetSerSerCysLysSerAlaArgIleGluThrSerCys 487  
Db 1174 GCTAATGAAAAATAATCAACA-----AAGATTGATTACAGTT 1212

QY 488 SerLeuLeuGluGlnThrGlnProAlaThrProSerLeuTyrLysAsnLysGluGlnHis 507  
Db 1213 TCA-----CCAGAGATATCATCTGATATGAAAGGTGAAGACGCTGAA 1254

QY 508 LeuSerGluAsnGluProValAspThrAsnSerAspAsnLeuPheThrAsp---Thr 526  
Db 1255 TTTACA-----GTCACAGTAAAGTATTCGACAGACGCGTTGAGCTTCAGT 1302

QY 527 AspLeuLysSerIleValLysAsnSerAlaSerLysSerHisAlaAlaGluLysLeuArg 546  
Db 1303 GATCTT-----TTAACAATAATATATCGTCTGTATCA-----GATGATTTAGT 1347

QY 547 SerAsnLysLysArgGluMetAspValAlaIleGluAspGluValLeuGluGlnLeu 566  
Db 1348 ACAATTTAAGCACTAACACGGTAAATCAAGATTGCGGAATCTACTATCAAGAAATTG 1407





## BEST AVAILABLE COPY

489 AATATACAAATGAACACCATACAGATTTACTGTGGCACTCAAAAAATGAACCTTTAAT 548  
176 rPheThrGluPheLeuLysAlaValGlnSerLysLysGlnProProGlnLeuSerPh 196  
549 TATTCGAGAGATGCTCAATAG-- 578  
196 eTyProProLeuAspGluProSerIleGlySerLysAsnValAspLeuSerGlyArgG1 216  
579 TGTTCCTGATCTCACAGAGAAGTGTATATACATACAGAAATGCTTTG----- 627  
216 nGluArgLysGlnIlePheLysGly---LysThrPheIlePheLeuAsnAlaLysGlnHi 235  
628 -----AAATGGATTACAAAGGAGAAAGAGAGAGAGCATTTATGAGAGAAACAAATGAA 680  
235 sLysLysLeuSer---SerAlaValPheGlyGlyGlyGluAlaArgLeuIleThrG1 254  
681 TCAAGAGAGCATGCTTCTCATACATCTTT-----AGGATGATTTTGA 725  
254 uGluAsnGluGluHisAsnPhePheLeuAlaProGlyThrCys----- 269  
726 AAGCAGAGAGAGAGGCTGAA-----CCTTCTAATTTGTGAAGGATCTGTAA 770  
270 -----ValValAsp----- 775  
771 GGTATCCATTTGATTTGGTTGATCTTGCAGGAGTGAAGAGCTGCTCAACAGCGC 830  
275 eThrAsnSerGlnThrLeuIleProAspCysGlnLysLysTrpIleGlnSerIleMetAs 295  
831 TGCAGGTGTCGG---CTCAAGGAGGCTGTAAT-----ATAATCGAAGCTTATT 878  
295 pMetLeuGlnArgGlnGlyLeuArgProIleProGluAlaGluLeuAlaValI1 315  
879 TATTTTG---GGACAAGTGATCAAGAACTTAGTGATGAGCAAGTGTGTTTCATA-- 933  
315 ePheMetThrThrLysAsnThrCysAspProGln----- 326  
934 -----AATATCGAGATAGCAAGTTAAACAGCAATCTTCCAGAAATCCCTT 977  
327 ---GlyHisProSerThrGly---LeuLysThrThrThrProGlyProSerLeuSerG1 344  
978 GGGAGGAAATCAAGACAGCTATTATCTGCACAAATCTCTCA----- 1020  
344 nGlyValSerValAspGluLysLeuMetProSerAlaProValAsnThr----- 360  
1021 ---GTATCTTTTGATGAACTCTTACTGCTCTCCAGTTTGCAGTACTGCTAAATATAT 1076  
361 ---ThrThrTyrrValAlaAspThrGluSerGluGlnAla----- 372  
1077 GAAGAACTACTCTTATGTTAATGAGGTATCACTGATGAGCTCTCTGAAAAGGTATAG 1136  
373 ---AspThrTrpAspLeuSerGluArgProLysGluLysValSerLysMetGluG1 391  
1137 AAAAGAAATAATGATCTTAAAAACAATTAAGAGGAGTT-----TCATTAGAGAC 1187  
391 nLysPheArgMetLeuSerGlnAsp-----AlaProThrValLysGluSerCysLysTh 409  
1188 CGGGCTCAGCAATGAAAAGAACCAATTGGCCCACTTTTGGAGAAAAGATTGCT 1247  
409 rSerSerAsnAsnSerMetValSerAsnThrLeuAlaLysMetArgIleProSerTy 429  
1248 TCAGAAAGTACAGATCAGAAATTAAGAAC---TTAACAGGATGCTGCTGCTTTC 1304  
429 rGlnLeuSerProThrLys----- 436  
1305 TTCCCTCAGCTTGCAACAGCAATTAAGGCTTAAAGGCTTAAAGAAACGAGATTACTTGGTGCCT 1364  
436 uProSerIleAsnLysSerLysAspArgAlaSerGlnGlnGlnThrAsnSerIleAr 456  
1365 TGGCAAAATTAACAAATTAAGAAC---TCAAACTATGCGAGATCAATTTAATATACCAAC 1421  
456 gAsnTyrrPheGlnProSerThrLys-----LysArgGluArgAspGluG1 471  
1422 AATATACAAACAAACAACTAAGCTTCTATATAATTTATTAGGAGAAATTCATGATC 1481

471 uAsnGlnGluMetSerSerCysLysSerAlaArgIleGluThrSerCysSerLeuLeuG1 491  
1482 TGCTCTGTTCAGAGCTGATGTTTTCATTAACACATCTTTGATACATTAAGTAGATA----- 1536  
491 uGlnThrGlnProAlaThrProSerLeuTrpLysAsnLysGluGlnHisLeuSerGluAs 511  
1537 -GAATGGAATCCAGCAACAAAGCTACTA-----AATCAGAGAAATATAGAAAGTGAGTT 1589  
511 nGluProValAspThrAsnSerAspAsnLeuPheThrAspThrAspLeuLysSerI1 531  
1590 GAATCTCCTCTGCTGCTGATCATTAATCTGTATTAGACTATCAACAACATCAGCAACAGA 1649  
531 eValLysAsnSerAlaSerLysSerHisAlaGluLysLeuArgSerAsnLysLysAr 551  
1650 AAAAAAAAATG-----GAATTTGAAATTAAGAAAGAA 1685  
551 gGluMetAspAspValAlaIleGluAspGluValLeuGluLysPheLysAspThrLys 571  
1686 TGATTTGGAT-----GAATTTGAGGCTCTAGAAAGAAACATAAAAGATCA 1733  
571 sProGluLeuGluLysValLysValGlnLysGlnGluLysValAsnValArgLys 591  
1734 A---GAGATGCAACTAATTCATGAATTTGCAACTTAAGAAATTTAGTTAAGCATCGAGA 1790  
591 sArgProArgMetAspIleGluThrAsnAspThrPheSerAspGluAlaValProGluSe 611  
1791 AGTATATATCAGATCTT----- 1809  
611 rSerLysIleSerGlnGluAsnGluLysLysArgGluLeu-----LysG1 628  
1810 -----GAGAATCAACTCAGTTTCAAAAGTAGAGCTGCTTAGAGAAAGGA 1853  
628 uAspSerLeuTrpSerAlaLysGluLysSerAsnAsnAspLysLeuGlnAsp----- 645  
1854 AGACCAAGATTAAAGAGCTACAGGATACATAGACTCTCAAAAGCTAGAAAATATAAAAT 1913  
646 -----AspSerGluMetLeuProLysLysLeuLeuLeuThrGluPh 659  
1914 GGACTTGTCTACTCTATTGGAAGAGCTTGAAGACCCAAACAATGAAGCAGACTCTGTT 1973  
659 eArgSerLeuValLysAsnSerThrSerArgAsnProSerGlyIleAsnAspAsp-- 678  
1974 TGATGCTGAAACTGTAGCCCTTGATGCCAAGAGAGAAATCAGCCTTTCTTAGAAGTGAAA 2033  
679 -----TyrrGlyLysLysAsn-- 684  
2034 TCTGGAGTTGAGGAGAAATGAAGAACTTGCAACTACATACAGCAAAATGGAATGA 2093  
684 ----- 684  
2094 TATTCAGTTATATCAAGCCNAATTGGAGCAAAAAGAAATCAAGTTGATCTGGAGAA 2153  
685 -----PheLysLysPheLysLysValThrTyrrProGlyAlaGlyLysLe 699  
2154 AGAATTAACAATCTGCTTTTAAATGAGATAACAAAACCTCACCTCCTCTATAGATGCAAGT 2213  
699 uProHisIleIleGlyGlySerAspLeuIleAlaHis-----HisAlaArgLysAsnTh 717  
2214 TCCA-----AAGATTGCTCTGTAATTTGGAATTTGGAAGGAAAGATTAC 2258  
717 rGluLeuGluGluTrpLeuArgGlnGluMetGluValGlnAsnGlnHisAlaLysGluG1 737  
2259 TGATCTTCAGAAAGAACTAATAAAGAGTTGAA---GAAATGAAGCTTTGGCGGAGAGA 2315  
737 u 737  
2316 A 2316

RESULT 5

US-09-643-597-119

; Sequence 119, Application US/09643597

; Patent No. 6426072



Qy 459 ----- 459  
Db 3755 ACTCGAAGACGAGCAATGTGAAAGAGGAACTTTGGTGGCAGAAATTAGAGTCTGA 3814  
Qy 460 -----GlnPr 461  
Db 3815 GAAAGCCATCAAGAGAGGAGTACGAGATTGAAAGGTTGAGGGTTCTACTGCAGGAAGA 3874  
Qy 461 oSerThrLysLysArgGluArgAspGluGlu -----AenGl 473  
Db 3875 AGCACCCGGAAGAGAGAAATATGAAATGAGCTGGCAAGGTAAAGAACCACTATATGA 3934  
Qy 473 nGluMetSerCysLysSerAlaArgIleGluThrSerCysSerLeuLeuGluGln 493  
Db 3935 GGAGATGAGTAATTTAAGAAC--AAGTATGAACAGAGATTAAACATTACGAAGACCAC 3991  
Qy 493 rGlnProAlaThrProSerLeuTrpLysAsnLysGluGlnHisLeuSerGluAsnGluPr 513  
Db 3992 CATCAAGGAGATA---TCCATGCAAAAAGAGGAGTATCCAAAATCTTAGAAACCCAG-- 4046  
Qy 513 oValAspThrAsnSerAspAsnLeuPheThrAspThrAspLeuLys---SerIleVa 532  
Db 4047 -CTTGATAGACTTTCAAGGGAAAT-----CGAGATCTGAAGGATGAATTTGT 4093  
Qy 532 lLysAsnSerAlaSerLysSerHisAlaAlaGluLysLeuArgSerAsnLysLysArgG1 552  
Db 4094 CAGGCTCAATCAGACATCTTCAGGCCACTGAGCAGCGAAGCGAGCTGAAGAAACGC 4153  
Qy 552 uMetAspAspValAlaIleGluAspGluValLeuGluLeuGlnLeuPheLysAspThrLysPr 572  
Db 4154 CCTTCAGCAAAAGCCCTGTGGCTCTGAGATAATCGAAG--AAAGCA 4198  
Qy 572 oGluLeuGluIleAspValLys---ValGlnLysGlnGluLysAspValAsnValArgLys 591  
Db 4199 GCATCTGGAGATAGAACTGAAGCAGGTCATGACGAGCGCTCTGAGGACAAATGCCGCA 4258  
Qy 591 sArgProArgMetAspIleGluThrAsnAspThr----- 602  
Db 4259 CAACGAGTCCCTGGAG--GAGGCTGCCAAGACCATTCAGGACAAAATAAGGAGATCGA 4315  
Qy 603 -----PheSerAspGluAlaValProGluSerSerLysLysSerGlnGl 617  
Db 4316 GAGACTCAAGCTGAGTTTTCAGGAGGAGGCC-----AAGCGCGCTGGGAATATGA 4366  
Qy 617 uAsnGluIleGlyLysLysArgGluLysGluLysGluAspSerLeuTrpSerAlaLys----- 635  
Db 4367 AATGAATGATGTAAGGTAAAGAAACAATTATGATGAGGAGATCATTTAGCTTAAAAAATCA 4426  
Qy 635 ----- 635  
Db 4427 GTTTGAGACCGAGATCAACATCACCAGACCCACCATCCACGAGCTCACCATGCAGAGGA 4486  
Qy 636 -GluIleSerAsnAsnAspLysLeuGlnAspAspSerGluMetLeuProLysLysLeuLe 655  
Db 4487 AGAGATACCACTAGTGGCTACCGGGCTCAGATAGACAACTCTACCCGAGAAAAACAGGAGCTT 4546  
Qy 655 uLeuThrGluPheArgSerLeuValIleLysAsnSer-----ThrSerArgAsnPr 672  
Db 4547 ATCTGAAGAAATAAAGAGGCTG-----AAGAACACTCTAACCCAGACCCACAGAGAATCT 4600  
Qy 672 oSerGlyIleAsnAspAspTyrrGlyGlnLeuLysAsnPhelLysLysPheLysValTh 692  
Db 4601 CAGGAGGGTGGAGAGACATCCACAG-----CAAAAGGCCAC 4639  
Qy 692 rTyProGlyAlaGlyLysLeuProHisIleIleGlySerAspLeuIleAlaHisHi 712  
Db 4640 T-----GGCTCTGAGGTG----- 4652  
Qy 712 sAlaArgLysAsnThrGluLeuGluGluTrpLeuArgGln-----GluMetGluValGl 730  
Db 4653 -TCTCAGAGGAAACAGCAGCTGGAGGTGAGCTGAGACAGTCACTCAGATGCCAACAGA 4711

Qy 730 nAsnGlnHisAlaLysGluGluSerLeuAlaAsp 741  
Db 4712 GGAGAGCGTAAGATATAAGCAATCTCTTGATGAT 4745  
RESULT 6  
US-09-480-884A-119  
; Sequence 119, Application US/09480884A  
; Patent No. 6482597  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Pan, Liqun  
; APPLICANT: Hosken, Nancy A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C6  
; CURRENT APPLICATION NUMBER: US/09/480, 884A  
; CURRENT FILING DATE: 2001-08-27  
; NUMBER OF SEQ ID NOS: 330  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 119  
; LENGTH: 8948  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-480-884A-119  
Alignment Scores: 1.44e-06 Length: 8948  
Pred. No.: 164.50 Matches: 187  
Score: 34.23% Conservative: 132  
Percent Similarity: 20.06% Mismatches: 295  
Best Local Similarity: 4.22% Indels: 319  
Query Match: 4 Gaps: 45  
DB: 45  
US-09-837-602-2 (1-754) x US-09-480-884A-119 (1-8948)  
Qy 2 TrpLysLeuLeuProAlaAlaGlyProAlaGlyGlyGluProTyrrArgLeuLeuThrGly 21  
Db 2331 TGGATGCTGATG-----GAGCTGCAGAAAGATTCCGAGGCAG 2366  
Qy 22 ValGluTrpValValGlyArgLysAsnCysAlaIleLeuLeuGluAsnAspGlnSerIle 41  
Db 2367 ATAGAGCAGCTCGCAGGCGAGGATGACTCTCAAAACCTCTTACAGACCCAGGGG--- 2423  
Qy 42 SerArgAsnHisAlaValLeuThrAlaAsn-----PheSerValThrAsnLeuSerGln 59  
Db 2424 TCTTCTCACCACATCAGAGTAAATTAACAGCTTAAGAGTGTGAGAGATGATTCACAA 2483  
Qy 60 ThrAspGluIleProValLeuThrLeuLysAspAsnSerLysTyrrGlyThrPheValAsn 79  
Db 2484 GCAATTGCTGAGGTCTCTCAACCAGCTTAAAGAT-----ATGCTTGCCAACCTTCAGAGGT 2537  
Qy 80 GluGluLys-----MetGlnAsn-----GlyPheSerArgThrLeuLysSer 93  
Db 2538 TCTGAAAGTACTGCTATTACAGAAATGAAGTATTTGGACTATTTCAGAACTCGAAAT 2597  
Qy 94 GlyAspGlyIleThrPheGlyValPheGlySerLysPheArgIleGluTyrrGluProLeu 113  
Db 2598 ATCAATGGTGTACAGATGGCTACTTAAATAGCTTATTCACAGTAAGG----- 2645  
Qy 114 ValAlaCysSerSerCysLeuAspValSerGlyLysThrAlaLeuAsnGlnAlaIleLeu 133  
Db 2646 -----GCACCTGCTCCAGGCTATTCTC 2666  
Qy 134 GlnLeuGlyGlyPheThrValAsnAsnTrpThrGluGluCysThrHisLeuValMetVal 153  
Db 2667 CAA-----ACAGAGACATG-----TTAAAGGTTTAT 2693  
Qy 154 SerValLysValThr-----IleLysThrIleCys-----AlaLeu 165  
Db 2694 GAAGCCAGGCTCACTGAGGAGGAACTGTCTGCTGACCTGGATAAGTGAAGCTTAC 2753



## BEST AVAILABLE COPY

Db 4653 -TCTCAGAGGAAACAGCAGCTGGAGGTGGAGTTCAGACAAAGTCACCTCAGATGCGAAGCAGA 4711  
 Qy 730 nAsnGlnHleAlaLysGluGluSerLeuAlaAsp 741  
 Db 4712 GGAGAGCGTAAGATATAAGCAATCTCTTGATGAT 4745

## RESULT 7

US-09-542-615A-119  
 ; Sequence 119, Application US/09542615A  
 ; Patent No. 6518256  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, Tongtong  
 ; APPLICANT: Fan, Liqun  
 ; APPLICANT: Kalos, Michael D.  
 ; APPLICANT: Bangur, Chaitanya S.  
 ; APPLICANT: Hosken, Nancy A.  
 ; APPLICANT: Fanger, Gary R.  
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY  
 ; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
 ; FILE REFERENCE: 210121.455C8  
 ; CURRENT APPLICATION NUMBER: US/09/542.615A  
 ; CURRENT FILING DATE: 2000-04-14  
 ; NUMBER OF SEQ ID NOS: 350  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 119  
 ; LENGTH: 8948  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-09-542-615A-119

## Alignment Scores:

Pred. No.: 1.44e-06 Length: 8948  
 Score: 164.50 Matches: 187  
 Percent Similarity: 34.23% Conservative: 132  
 Best Local Similarity: 20.06% Mismatches: 295  
 Query Match: 4.22% Indels: 319  
 Gaps: 45

US-09-837-602-2 (1-754) x US-09-542-615A-119 (1-8948)

Qy 2 TrpLysLeuLeuProAlaGlyProAlaGlyGluProTyrArgLeuLeuThrGly 21  
 Db 2331 TGGATGCTGATG-----GAGCTGCAGAGATTCGCGAGCAG 2366  
 Qy 22 ValGluTyrValValGlyArgLysAsnCysAlaLeuLeuGluAsnAspGlnSerIle 41  
 Db 2367 ATAGAGCAGCTGGCGGCGAGGATGACTCTCAAAAACCTCCCTCTAGCAGACCGGG--- 2423  
 Qy 42 SerArgAsnHisAlaValLeuThrAlaAsn-----PheSerValThrAsnLeuSerGln 59  
 Db 2424 TCTTCTCACCACATCACAGTGAATTAACGAGCTTAAGAGTGTGCGAGAATGATTTCACAA 2483  
 Qy 60 ThrAspGluIleProValLeuThrLeuLysAspAsnSerLysTyrGlyThrPheValAsn 79  
 Db 2484 GCAATTTGCTGAGTTCTCAACAGCTTAAAGAT-----ATGCTTGGCCAACTTCAGAGGT 2537  
 Qy 80 GluGluLys-----MetGlnAsn-----GlyPheSerArgThrLeuLysSer 93  
 Db 2538 TCTGAAAGTACTGCTATTTCACAGATGAAGTATTGGACTATTTCAGAACTGGAAT 2597  
 Qy 94 GlyAspGlyIleThrPheGlyValPheGlySerLysPheArgIleGluTyrGluProLeu 113  
 Db 2598 ATCAATGGTGTACAGATGGCTACTTAAATAGCTTATGACAGTAAG----- 2645  
 Qy 114 ValAlaCysSerSerCysLeuAspValSerGlyLysThrAlaLeuAsnGlnAlaLeu 133  
 Db 2646 -----GCACCTGCTCCAGGCTATTCTC 2666  
 Qy 134 GlnLeuGlyGlyPheThrValAsnAsnTrpThrGluGluCysThrHisLeuValMetVal 153  
 Db 2667 CAA-----ACAGAGACATG-----TTAAGGTTTAT 2693  
 Qy 154 SerValLysValThr---IleLysThrIleCys-----AlaLeu 165

Db 2694 GAAGCAGGCTCACTGAGGAGGAAACTGTCTGCTGGACCTGGATAAAAGTGAAGCTTAC 2753  
 Qy 166 IleCysGlyArgProIleValLysProGlu----- 175  
 Db 2754 CGCTGTGGACTGAAGAAATAAAATGACTTGAACCTTGAAGAAGTCGTTGTGGCACT 2813  
 Qy 176 TyrPheThrGluPheLeuLysAlaValGlnSerLysLysGlnProProGlnIleGluSer 195  
 Db 2814 ATGAAGACAGAACTACAGAAAGCCAGCAGATCCACTCTCAGACTTCACAGCAGTATCCA 2873  
 Qy 196 PheTyrProProLeuAspGluProSerIleGlySerLysAsnValAspLeuSerGlyArg 215  
 Db 2874 CTTTAT---GATCTGACTTGGCGCAAGTTCGGTGAAGAAAGTCACACAGCTGACAGACCGC 2930  
 Qy 216 GlnGluArg-----LysGlnIlePhe 222  
 Db 2931 TGGCAAGGATAGATAAACAGATCGACTTTAGATTATGGACCTGGAGAAACAATCAAG 2990  
 Qy 223 LysGlyLysThrPhe-----IlePheLeuAsnAla 232  
 Db 2991 CAATTGAGGAATTATCGTGAATACTATCAGGCTTTCTGCAAGTGGCTCTATGATCGTAA 3050  
 Qy 233 LysGlnHisLysLysLeuSerSerAlaValPheGlyGlyGlyGluAlaArgLeuIle 252  
 Db 3051 CGCCGCGAGGATTCCTTAGAATCCATGAAATTT---GGAGATTCCAACACAGTC 3101  
 Qy 253 ThrGluGluAsnGluGluHisAsnPhePheLeuAlaProGlyThrCysValValAsp 272  
 Db 3102 ATGCGGTTTTGAATGAGCAGCAAGAACTTG----- 3131  
 Qy 273 ThrGlyIleThrAsnSerGlnThrLeuIleProAspCysGlnLysLysTrpIleGlnSer 292  
 Db 3132 -----CACAGTGAATATCTGGCAACGAGACAAATCAGAGGAAGTACAAAA 3179  
 Qy 293 IleMetAspMetLeuGlnArgGlnGlyLeuArgProIleProGluAlaGluIleGlyLeu 312  
 Db 3180 ATTGCTGAACCTTTCGCGCAATTCA-----ATTAAAGATTATGAGCTCCAGCTG 3227  
 Qy 313 AlaValIlePheMetThrThrLysAsnTyrCysAspProGlnGlyHisProSerThrGly 332  
 Db 3228 GCC-----TCATAC-----ACTCAGGA 3245  
 Qy 333 LeuLysThrThrThrProGlyPro-----SerLeuSerGlnGlyVal 346  
 Db 3246 CTGGAACCTCTGCTGAACATACCTATCAAGAGGACCATGATTTCAGTCCCTCTTGGGGTG 3305  
 Qy 347 SerValAspGluLysLeuMetProSerAlaProValAsnThrThrThrThrValAlaAsp 366  
 Db 3306 ATTCTGCAAGAGGC-TGCAGATGTTTCATGCTCGGTACATTGAACCTACTTAC----- 3355  
 Qy 367 ThrGluSerGluGlnAlaAspThrTip-Asp-----LeuSerGluArgProLy 382  
 Db 3356 -----AAGATCTGGAGACTATTACAGGTTCTTAAGTGAGTGCTGAA 3397  
 Qy 382 sGluIleLysValSerLysMetGluGln-----LysPheArgMetLeuSerGlnAspAlaPr 401  
 Db 3398 GAGTTTGGAGAGCTGAAGCTGAAAAATACCAAGATCGAAGTTTGGAGAGGAGCTCAG 3457  
 Qy 401 oThrValLysGluSerCysLysThrSerSerAsnAsnAsnSerMetValSerAsnThrLe 421  
 Db 3458 ACTGCCCGAGATGCCAACTCGGAAAACTGTGAATAAGAACAAATTCCTGGATCAGAACCT 3517  
 Qy 421 uAlaLysMetArgIleProAsnTyrGlnLeuSerProThrLysLeuProSerIleAsnLy 441  
 Db 3518 GCAGAAATACAGCAGAGTGTCCCGATTCAAA---GCCAAGCTTCGAGCCTGGAGGA 3574  
 Qy 441 sSerLysAspArgAla----- 446  
 Db 3575 GCTGAAGAGACAGGCTGAGCTGGATGGAGTGGGAACTCGGCTAAGCAAAATCTAGACAAAGTGCTA 3634  
 Qy 447 -----SerG1 448  
 ;

## BEST AVAILABLE COPY

Db 3635 CGGCCAAATAAAGAACTCAATGAGAGAGATCACCGCACTGATCTTATGAGATTGAGATGA 3694  
Qy 448 nGlnGlnGlnThrAsnSerIleArgAsnTyrPhe----- 459  
Db 3695 AAAGAGAAGAGAAATCTGTGGAAGACAGATTTGACCAACAGAGAAGATGACTATGACCA 3754  
Qy 459 ----- 459  
Db 3755 ACTGAGAAAGCAAGGCAATCTGAAAGAGAGAACCTTGGTTGGCAGAAATTAGAGTCTGA 3814  
Qy 460 -----GlnPr 461  
Db 3815 GAAAGCCATCAAGAGAGAGAGTAGAGATTTGAAAGGTTGAGGGTTCTACTGCGAGGAGA 3874  
Qy 461 oSerThrIlyslsArgGluArgAspGluGlu-----AsnG1 473  
Db 3875 AGGCACCGGAGAGAGATATGAAATGAGCTGCGAAAGGTAAAGAACCACTATATGA 3934  
Qy 473 nGluMetSerSerCysIlyslsSerAlaArgIleGluThrSerCysSerLeuLeuGluGlnTh 493  
Db 3935 GGAGATGAGTAATTTAAGGAAC---AAGTATGAAACAGAGATTAACTATTCAGAGACCAC 3991  
Qy 493 rGlnProAlaThrProSerLeuTrpIysAsnLysGluGlnHisLeuSerGluAsnGluPr 513  
Db 3992 CATCAAGAGATA---TCCATGCAAAAGAGGATGATTCCAAAATCTTGAAGAACCG-- 4046  
Qy 513 oValAspThrAsnSerAspAsnLeuPheThrAspThrAspLeuLys---SerIleVa 532  
Db 4047 -CTTGATAGATTTCAAGGGAAT-----CGAGATCTGAAGGATGAATGT 4093  
Qy 532 lIysAsnSerAlaSerIlyslsSerHisAlaGluLysLeuArgSerAsnLysArgG1 552  
Db 4094 CAGGCTCAATCAGCAGCATCTTCAGCGCACTGAGCAGCGAAGCGAGCTGAAGAAACGC 4153  
Qy 552 uMetAspAspValAlaIleGluAspGluValLeuGluGlnLeuPheIlyslsAspThrLysPr 572  
Db 4154 CTTTCAGCAAAAGCGCTGTGCTCTGAGATAATCGAAG-----AAGCA 4198  
Qy 572 oGluLeuGluIleAspValLys---ValGlnLysGlnGluAspValAsnValArgLy 591  
Db 4199 GCATCTGGAGATAGACTGAGAGCGGTCTATCGCAGCGGCTCTGAGGACATGCCGGCA 4258  
Qy 591 sArgProArgMetAspIleGluThrAsnAspThr----- 602  
Db 4259 CAAGCAGTCCCTGGAG---GAGGCTGCCAAGCACTTCAGGACAAAATAAGGAGATCGA 4315  
Qy 603 -----PheSerAspGluAlaValProGluSerSerIlyslsIleSerGlnG1 617  
Db 4316 GAGACTCAAGCTGAGTTTTCAGGAGGAGGCC-----AAGCGCCGCTCGGGAATATGA 4366  
Qy 617 uAsnGluIleGlyLysLysArgGluLeuLysGluAspSerLeuTrpSerAlaLys----- 635  
Db 4367 AATGTACTGATAGGTAAAGAAACAATTATGATGAGGAGATCATAGCTTAAATAATCA 4426  
Qy 635 ----- 635  
Db 4427 GTTTGAGACCGAGATCAACATCACCAAGCACCATCCACCAGCTCACCATGCAGAAGGA 4486  
Qy 636 -GluIleSerAsnAsnAspLysLeuGlnAspAspSerGluMetLeuProLysLysLeuLe 655  
Db 4487 AGAGATACCACTAGTGGCTACCGGGCTCAGATAGACAAATCTCACCCGAGAAAACAGAGCTT 4546  
Qy 655 uLeuThrGluPheArgSerLeuValIleIysAsnSer-----ThrSerArgAsnPr 672  
Db 4547 ATCTGAAGAAATAAGAGCGTG-----AAGAAACACTTAACCCAGACCAAGAGAAATCT 4600  
Qy 672 oSerGlyIleAsnAspAspTyrGlyGlnLeuLysAsnPheIlyslsValTh 692  
Db 4601 CAGGAGGTGGAGAGACATCCCAACAG-----CAAAAGGCCAC 4639  
Qy 692 rTyProGlyAlaGlyLysLeuProHisIleIleGlySerAspLeuIleAlaHisH1 712  
Db 4640 T-----GGCTCTGAGGTG----- 4652

Qy 712 sAlaArgLysAsnThrGluLeuGluGluTrpLeuArgGln-----GluMetGluValG1 730  
Db 4653 -TCTCAGAGGAAACAGCAGCTGGAGGTTGAGTGGAGACAAGTCACTCAGATGCCAAGCA 4711  
Qy 730 nAsnGlnHisAlaLysGluGluSerLeuAlaAsp 741  
Db 4712 GGAGAGCGTAAGATATTAAGCAATCTCTTTGATGAT 4745

## RESULT 8

US-09-606-421B-119  
; Sequence 119, Application US/09606421B  
; Patent No. 6531315  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangut, Chaitanya S.  
; APPLICANT: Hoeken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Steiky, Yasar A.W.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C9  
; CURRENT APPLICATION NUMBER: US/09/606.421B  
; CURRENT FILING DATE: 2000-06-28  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 119  
; LENGTH: 8948  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-606-421B-119

Alignment Scores:  
Pred. No.: 1.44e-06 Length: 8948  
Score: 164.50 Matches: 187  
Percent Similarity: 34.23% Conservative: 132  
Best Local Similarity: 20.06% Mismatches: 295  
Query Match: 4.22% Indels: 319  
DB: 4 Gaps: 45

US-09-837-602-2 (1-754) x US-09-606-421B-119 (1-8948)

Qy 2 TrpLysLeuLeuProAlaAlaGlyProAlaGlyGluProTyrArgLeuLeuThrGly 21  
Db 2331 TGGATGCTGATG-----GAGCTGCAGAAAGATTTCGAGGCAG 2366  
Qy 22 ValGluTrpValValGlyArgLysAsnCysAlaIleLeuIleGluAsnAspGlnSerIle 41  
Db 2367 ATAGACACTCGCGAGGCGAGATGACTCTCAAAACCTCCCTCTAGCAGACAGGGG--- 2423  
Qy 42 SerArgAsnHisAlaValLeuThrAlaAsn-----PheSerValThrAsnLeuSerGln 59  
Db 2424 TCTTCTCACCACATCAGTCAAGTAAACGAGTAAAGAGTGGCAGATGATTCACAA 2483  
Qy 60 ThrAspGluIleProValLeuThrLeuLysAspAsnSerIlyslsTyrGlyThrPheValasn 79  
Db 2484 GCAATTCGTGAGGTCTCTCAACAGCTTAAAGAT-----ATGCTTGCCAACCTTCAGAGGT 2537  
Qy 80 GluGluLys-----MetGlnAsn-----GlyPheSerArgThrLeuLysSer 93  
Db 2538 TCTGAAAAGTACTGCTATTATTACAGAAATGAAGTATTTGGACTATTTCAGAAACTGGAAT 2597  
Qy 94 GlyAspGlyIleThrPheGlyValPheGlySerLysPheArgIleGluTyrGluProleu 113  
Db 2598 ATCAATGGTGTACAGATGGCTACTTAATAGCTTATTCACACAGTAAGG----- 2645  
Qy 114 ValAlaCysSerSerCysLeuAspValSerGlyLysThrAlaLeuAsnGlnAlaIleLeu 133  
Db 2646 -----GCACCTGCCAGGCTATTCTC 2666







Qy 429 rGlnLeuSerProThrLys - - - - - Le 436  
| | | | | : : : : :  
Db 1305 TTCCCTCAGCGTGCACAGCAATTAAGGCTAAAGAAAGAGAGAGTACTTGGTGCCT 1364  
Qy 436 uProSerIleAsnLysSerLysAspArgAlaSerGlnGlnGlnThrAsnSerIleAr 456  
| | | | | : : : : :  
Db 1365 TGGCAAAATTAACAAAATGAAGAAC--TCAAACTATGCAGATCAATTTAATATACCAAC 1421  
Qy 456 gAsnTyrPheGlnProSerThrLys - - - - - LysArgGluArgAspGluG1 471  
| | | | | : : : : :  
Db 1422 AAATATACAAACAAACATAGCTTCTATAAATTTATACGAGAAATTTGATGAATC 1481  
Qy 471 uAsnGlnGluMetSerCysLysSerAlaArgIleGluThrSerCysSerLeuLeuG1 491  
| | | | | : : : : :  
Db 1482 TGCTGTCTCAGAGTCTGATGTTTCAGTAACTCTTGATACATTAAGTGAGATA-- 1536  
Qy 491 uGlnThrGlnProAlaThrProSerLeuTrpLysAsnLysGlnHisLeuSerGluAs 511  
| | | | | : : : : :  
Db 1537 -GAATGGAATCCAGCAACAAAGCTACTA--AAATCAGGAGAAATATAGAAAGTGAGTT 1589  
Qy 511 nGluProValAspThrAsnSerAspAsnAsnLeuPheThrAspThrAspLeuLysSerI1 531  
| | | | | : : : : :  
Db 1590 GAATCTACTTCGTCTGACTATGATAATCTGTTATAGACTATGAACTACGAAACA-- 1647  
Qy 531 eValLysAsnSerAlaSerLysSerHisAlaAlaGluLysLeuArgSerAsnLysLysAr 551  
| | | | | : : : : :  
Db 1648 - - - - - GAAAGAGAGAAATGGAATTAATAA--GAAAGAGAA 1685  
Qy 551 gGluMetAspAspValAlaLleGluAspGluValLeuGlnLeuPheLysAspThrLys 571  
| | | | | : : : : :  
Db 1686 TGATTTGGAT - - - - - GAATTTGAGGCTCTAGAAAGAAATAAAGAGATCA 1733  
Qy 571 sProGluLeuGluLeuAspValLysValGlnLysGlnGluAspValAsnValArgLys 591  
| | | | | : : : : :  
Db 1734 A--GAGATGCAACTAATTCATGAATTTGAACTTAAAGAAATTTAGTTAAGCATCGAGA 1790  
Qy 591 sArgProArgMetAspIleGluThrAsnAspThrPheSerAspGluAlaValProGluSe 611  
| | | | | : : : : :  
Db 1791 AGTATATAATCAAGATCTT - - - - - 1809  
Qy 611 rSerLysIleSerGlnGluAsnGluLeuGlyLysArgGluLeu - - - - - LysG1 628  
| | | | | : : : : :  
Db 1810 - - - - - GAGATGAAGTCACTCAGTTCAAAAGTAGAGTAGCTGCTTAGAGAGAAAGGA 1853  
Qy 628 uAspSerLeuTrpSerAlaLysGluIleSerAsnAsnAspLysLeuGlnAsp - - - - - 645  
| | | | | : : : : :  
Db 1854 AGACAGATTAAGAAGCTACAGGAATACATAGACTCTCAAAAGCTAGAAAATATAAAAT 1913  
Qy 646 - - - - - AspSerGluMetLeuProLysLysLeuLeuLeuThrGluPh 659  
| | | | | : : : : :  
Db 1914 GGACTTGTCTACTCATTTGGAAGAGNTTGAAGACCCAAACAAATGAAGCAGACTCTGTT 1973  
Qy 659 eArgSerLeuValLleLysAsnSerThrSerArgAsnProSerGlyLysLeuAspAsp-- 678  
| | | | | : : : : :  
Db 1974 TGATGCTGAAACTGTAGCCCTTGATGCCAAGAGAGAAATCAGCCCTTCTTAGAAGTGAAGA 2033  
Qy 679 - - - - - TyrGlyGlnLysAsn-- 684  
| | | | | : : : : :  
Db 2034 TCTGGAGTTGAAGAGAAATGAAGAAGTCTGCACTACATACAGCAATGGAAGAAATGA 2093  
Qy 684 - - - - - 684  
Db 2094 TATTCAGTTATACAAAGCCAAATGGAGGCAAAAGAAATGCAAGTTGATCTGGAGAA 2153  
Qy 685 - - - - - PheLysLysPheLysValThrTyrProGlyAlaGlyLysLe 699  
| | | | | : : : : :  
Db 2154 AGAATTACAATCTGCTTTTAAATAGATAACAAAACCTCACCTCCCTTATAGATGCAAAAT 2213  
Qy 699 uProHisIleIleGlyGlySerAspLeuIleAlaHis - - - - - HisAlaArgLysAsnTh 717  
| | | | | : : : : :  
Db 2214 TCCA - - - - - AAAGATTTGCTCTGTAATTTGGAAATTTGGAGGACATGACTGTCAAAGCT 3057

Qy 717 rGluLeuGluGluTrpLeuArgGlnGluMetGluValGlnAsnGlnHisAlaLysGluG1 737  
| | | | | : : : : :  
Db 2259 TGATCTTCAGAAAGAACTAAATAAGAGAGTTGAA--GAAATGAAGCTTTTGGCGGAAGA 2315  
Qy 737 u 737  
| | | | | : : : : :  
Db 2316 A 2316  
RESULT 10  
US-09-220-132-79  
; Sequence 79, Application US/09220132  
; Patent No. 6506607  
; GENERAL INFORMATION:  
; APPLICANT: Shivjan, Andrew W.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT  
; OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCES: 07334-074001  
; CURRENT APPLICATION NUMBER: US/09/220,132  
; CURRENT FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: US 60/079,303  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: US 60/068,821  
; PRIOR FILING DATE: 1997-12-24  
; NUMBER OF SEQ ID NOS: 191  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 79  
; LENGTH: 5857  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-220-132-79  
Alignment Scores:  
Pred. No.: 1,16e-06 Length: 5857  
Score: 162.50 Matches: 101  
Percent Similarity: 37.50% Conservative: 82  
Best Local Similarity: 20.70% Mismatches: 176  
Query Match: 4.17% Indels: 129  
DB: 4 Gaps: 19  
US-09-837-602-2 (1-754) x US-09-220-132-79 (1-5857)

Qy 333 LeuLysThrThrThrProGlyProSerLeuSerGlnGlyValSerValAspGluLysLeu 352  
| | | | | : : : : :  
Db 2587 CTAAAGCTTACTAACCTTCAGGAAAATTTGAGTCAAGTCAAGTGAAGAGACTTTG 2646  
Qy 353 MetProSerAlaProValAsnThrThrThrTyrValAlaAspThrGluSerGluAla 372  
| | | | | : : : : :  
Db 2647 GAAAAAGAACTTCAGATTTTGAAGAAAAAGTTTGCT--GAAGCTTCAGAGAGGCA 2700  
Qy 373 AspThrTrpAspLeuSerGluArgProLysGluLysValSerLysMetGluGlnLys 392  
| | | | | : : : : :  
Db 2701 GTCTCTGTTTCAGAGAGATATGCAAGAACTGTAATTAAGTTACACCAAGAGGAGAACAG 2760  
Qy 393 PheArgMetLeuSerGlnAspAlaProThrValLysGluSer - - - - - 406  
| | | | | : : : : :  
Db 2761 TTTAAACATGCTGCTCTGCTGCTGAGAGAGCTGAGAGAAACTTAGCAGATATGAGGCA 2820  
Qy 406 - - - - - 406  
Db 2821 AAATTTAGAGAGAAAGATGAGAGAGAGAGAGAGCTGATAAGGCAAAAGGAAACTGGAA 2880  
Qy 407 - - - - - CysLysThrSerSerAsnAsnSerMetValSerAsnThr 420  
| | | | | : : : : :  
Db 2881 AATCAGATTCAGAAATAATGAAGATGCTCAGGAGATACTTCTCTCAGCTGACAAAAATG 2940  
Qy 421 LeuAlaLysMetArgIleProAsnTyrGlnLeuSerProThrLysLeuProSerIleAsn 440  
| | | | | : : : : :  
Db 2941 AAGCATGAATTAGCTCTGAAAGAAAGAGATGTAGAGAAATTTACAGCTA--AAACTTACA 2997  
Qy 441 LysSerLysAspArgAlaSerGlnGlnGln - - - - - ThrAsnSerIle 455  
| | | | | : : : : :  
Db 2998 AAGCTAATGAAATGAAGTTTCTGCAAAAAAGTATTGAGGACATGACTGTCAAAGCT 3057



QY	117	rSerCysLeuaspValSerGlyLysThrAlaLeuasnGlnAlaIleLeuGlnLeuGlyCl	137
DB	379	-GAAATAAAACAATATCACAAACAGTACAGACAGATCAGTTGATCAGAGA	432
QY	137	yPheThrValAsnAenTpThrGluGlyCysThrHisLeuVal	151
DB	433	-----ATGAATCTCGATCGGAACAGTTTTCTCAATCGTTTTACTACCC	485
QY	152	-----MetValSerValLysValThrIleLysThrIleCysAlaLeuIleC	167
DB	486	ATTCGGTAATTTTTTGGTTTCATCAAGCAGTATGAAGAGACTGTTTAC	545
QY	167	sgIlyArgProIleValLysProGluTyPheThrGluPheLeuLysAlaValGlnSerIy	187
DB	546	CGGTACTCAATTTTC-----CAACAGTTCAATGAGCGATTAAAAAGAA	596
QY	187	slYsglnProProGlnIleGluSerPhe-----	196
DB	597	ACAAACAGCA-ACAAAAATTGGATCATTTAGACGAAGAGCTGCATCTT	655
QY	197	-----	201
DB	656	TTGTTTTAGTCAAGAAGAGCAACACGAGCAGGGTTTGAAGCCGTTTT	715
QY	201	pGluProSerIleGlySerLysAsnValAspLeuSerGlyArgGlnGluArgLysGlnI	221
DB	716	CAAACCATCA--GGCAATCTCGAAAAACAATCAGCGAAGAAAAAGAAAG	772
QY	221	ePheLysGlyLysThr-----PheIlePheLeuAsnAlaLysGlnHisL	236
DB	773	AACTTCAGGAAAAACAAAGCAACTAGAAAAATTCCTACTATCGTTTGA	832
QY	236	slYsLeu-SerSerAlaValPheGlyGlyGluAlaArgLeulleThrGluGluA	256
DB	833	AAAGTTATGAAGAAAAACGGATTATTAATAAACAGCAAGAAAGAAATTA	892
QY	256	snGluGluGluHisAsnPhePheLeuAlaProGlyThrCysValAspThrGlyIle	276
DB	893	ACGAAATAGAGAA-----	906
QY	276	hrAsnSerGlnThrLeulleProAspCysGlnLysLysTrpIle-----	290
DB	907	-----AAGAACGATGATGGGTATTATGAAATTA	937
QY	291	--GlnSerIleMetAspMetIeuGlnArgGlnGlyLeuArgProIleProGluAlaGluI	310
DB	938	CGCAACGAGTATAGTCCAAATCCAGCGC-----CTACAGAAATAAAAG	991
QY	310	leGlyLeuAla-----ValIlePheMetThrThrLysAsnT	322
DB	992	TAGAACTGTCAAAAAAGTAGTGAGCNAACAAGAAACTAGCGATGATCAG	1051
QY	322	yrCysAspProGlnGlyHisProSerThrGlyLeuLysThrThrThrProGlyProSerL	342
DB	1052	ATGAAGAGTGGCAAAAAAATGAAGCAACCGGTACGCCGACAAACAACA	1111
QY	342	euSerGlnGlyValSerValAspGlnLysLeuMetProSerAlaPro-----	357
DB	1112	CTGCTCAAAACCTCAAAACAAACAGATGATGGTGCCAAATTGTCCAA	1171
QY	357	-----	357
DB	1172	AAAAACAAGCGCAACAATTAACAATTTTCATTGGATAAAGAAATTTGA	1231
QY	358	-----ValAsnThrThrThrTyrValAlaAspThrGluSerGluGlnAlaAspThr	375
DB	1232	AGCTGTATCAAAATCTCGTATCTATCATCAGGAAGAACTCGAATCTT	1291
QY	375	rpAsp-----	379
DB	1292	TGGATCAGGAAAACTGAAGAAGATCGTCTGCTTTGGACAGCTTAAATAT	1351

QY	379	luArgProLysGluIleLys-	-----ValSerLysMetG 390
DB	1352	AAAAAGCAGCAAAATAGAAAAA	-----GCTGCTCGCAGACAGATAA 1411
QY	390	luGlnLysPheArgMetLeuSerGlnAspAlaProThrValLysGluSerCysLysThrS	410
DB	1412	GAGAAAGAACTCAAAAAGCACTGAAGAAATACAAAAATAGTCACCTATTGAAGAAC	1471
QY	410	erSerAsnAsnAsnSerMetValSerAsnThrLeuAlaLysMetArgIleProAsnTyArg	430
DB	1472	AGACAGAACAAAGCAGAAACAGCTGAAAGCCAATGGCGAAAGCAGCAAAATGCTCGTCTTC	1531
QY	430	lnLeu-	-----S 432
DB	1532	AGCTTTTTCGCTCAGGGGAGCCATGCTTGTTGTGGATCAACGGAAACACCCCATAC	1591
QY	432	erProThrLysLeuProSerIleAsnLysSerLysAspArgAlaSerGlnGlnGln	450
DB	1592	AACAATTAACACGAAACAGCCAAATTAAGGAAGATATCTTAAAAAGTAGAACACAACTGG	1651
QY	451	--GlnThrAsnSerIleArgAsnTyPheGlnProSerThrLysLysArgGluArgAspG	470
DB	1652	CAGAAGCTGAGTCGCTGTAGAAGAAGAACTCAGCAAAATCATTTGCCAAAGTGAAGACCATG	1711
QY	470	luGluAsn-----GlnGluMetSerSerCysLysSerAlaArgIleGluThrSerCysS	488
DB	1712	AAAATAATCTTCAACACAAATATCATGATTAGAACAAAAAANTCATGGCAACGAATATAC	1771
QY	488	erLeuLeuGluGlnThrGln-----ProAlaThrProSerLeuT	501
DB	1772	AATTGGCTGAACAGAGAACACACTTGCAACAGGCTTTGAAAAAGGCATTTCTCTGAGATA	1831
QY	501	rpLysAsnLys-	-----S 504
DB	1832	CAGAACAAAAACAAAAACAACCTCTGTAGTAATCGAACAACTTTAGATAGACGAAAA	1891
QY	505	-----G 505	
DB	1892	GCAAGATGGCAATGCAAGAAATAGAGCTGGAAGAAATAGACAAACAAGCAGAAAAAGCTCG	1951
QY	505	luGlnHisLeuSerGluAsnGluProValAspThrAsnSerAspAsnAsnLeu--PheT	524
DB	1952	AACCAAAATAGCTGTCTACAAACAGCAGCAGACAGAAAAATAATACGCTCCAGCAAC	2011
QY	524	hrAspThrAspLeuLysSerIle-----ValLysAsnSerAlaSerLysSerHisA	541
DB	2012	TGCAAGCAGAAAAATCAAAAGTTTAGAACAAACAATGGCAAGATACGGATAGTAAGCTTTAG	2071
QY	541	laalaGluLysLeuArgSerAsnLysLysArgGluMetAsp-----AspValAlaIleG	559
DB	2072	AAGAGGAGATACGACGACTTGAAAAACAGTTAGAAAGAACCTCAACTACACTAGCTGTTG	2131
QY	559	luAspGluValLeuGluGlnLeuPheLysAsp-----ThrLysProGluL	574
DB	2132	AGCAGAAGCAGGAGTGCAATGTTTGCAGATCTTTCATACGCTTCGACACAGCTTGATC	2191
QY	574	euGlu-----IleAspValLysValGlnLysGlnGluAspValA	588
DB	2192	TTCAACATGAACAAATAGAAAAAATAGATCAAAAAATAGAAAGGAACAAAGAAAGATAG	2251
QY	588	snVal-----S 589	
DB	2252	CTAAAAAGTTAGAAAGCCAGTCGTATTTTTCACAAATGAAGAAATCTGTGCATTTGAC	2311
QY	589	-----S 589	
DB	2312	AACAGCAAGCACAAATATAAGAAAAACCAACGTACAGTTACTTCTTATCATGAAGACCAAT	2371
QY	590	-----ArgLysArgProArgMetAspIleGluThrAsnAspThrPheSerA	605
DB	2372	TAGTGACAGCTGACCGGCTGCGTCAATTAGAAAAATATCCAGCTTAACCTGAGACATTC	2427
QY	605	spGluAlaValProGluSerSerLysIleSerGlnGlu--AsnGluIleGluLysLysA	624

Db 2428 -----CNGATACAGAGATACCCACAGTTAGAGAAATAGACGTATGA 2476  
Qy 624 rgGluLeuLysGluAspSerLeuTrpSerAlaLysGluLeuSer---AsnAsnAspLysL 643  
Db 2477 TCGAATAAAGCAAGAAAGATATACGGTTTACAGAGACAAATAATAGTAAATCAAAAA 2536  
Qy 643 euGlnAspSerGluMetLeuProLysLysLeuLeuLeuThrGluPheArgSerLeuV 663  
Db 2537 TCTACGAT-----GAATGCTTTTCGATTT 2560  
Qy 663 alileLysAsnSerThrSerArgAsnProSerGlylleAsnAspAspTyrGlyGlnLeuL 683  
Db 2561 ATCACACAGCCAGACGAATTA-----GATGAGCTTACGCAATAC 2602  
Qy 683 ysnPheLysPheLysValThrTyrProGlyValaGlyLysLeuProHisileI 703  
Db 2603 AGCAGCTTTCGCA-----ACATTCAACGAGAGAAATCCT----- 2637  
Qy 703 leGlyGlySerAspLeuileAlahHisAlaArgLysAsnThrGluLeuGlu----- 721  
Db 2638 -----AAGAAGACTAGTTTGGACGGTATG 2662  
Qy 722 -----TrpLeuArgGlnGluMetGluValGlnAsnGlnHisAlaLys----- 735  
Db 2663 TGCTTCAGGTTTATCTTCAAGAGTGTACAGTAGCAAAATGATCATCTCCAAGCTTTAA 2722  
Qy 736 -----GluGluSerLeuAlaAspLeuPheArgTyr 746  
Db 2723 CGAAATCGTTATCATTTGAGCTAGCGATACCATTCGCAGTTAT 2769

## RESULT 12

US-08-923-992A-7  
Sequence 7, Application US/08923992A  
Patent No. 6280738  
GENERAL INFORMATION:  
APPLICANT: Tai, Joseph Y.  
APPLICANT: Blake, Milan S.  
TITLE OF INVENTION: No. 6280738-IGA Fc Binding Forms of the Group B  
TITLE OF INVENTION: Streptococcal Beta Antigens  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/923, 992A  
APPLICATION NUMBER: US/08-923, 992A  
FILING DATE: 05-SEP-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/024,707  
FILING DATE: 06-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1438.0140001/RWE  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3294 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..3294  
US-08-923-992A-7  
Alignment Scores:  
Pred. No.: 6.39e-07 Length: 3294  
Score: 161.00 Matches: 141  
Percent Similarity: 37.11% Conservative: 124  
Best Local Similarity: 19.75% Mismatches: 233  
Query Match: 4.13% Indels: 216  
DB: 3 Gaps: 39  
US-09-837-602-2 (1-754) x US-08-923-992A-7 (1-3294)  
Qy 192 GlnileGluSerPheTyrProLeuAspGluProSerileGlySerLysAsnValasp 211  
Db 298 CAGAAAATGAGTTTAAACAAAATTTGATGAACAAATGATCTGATGATTTAGAA 357  
Qy 212 LeuSerGlyArg-----GlnGluArgLysGlnile 221  
Db 358 TTAGAAAATCAATTTAAACGAACTAATAGACTGTTACACATCAACACATGAAGAAGTT 417  
Qy 222 PheLysGlyLysThrPheLysPheLeuAsnAlaLysGlnHisLysLysLeuSerSerAla 241  
Db 418 GAGAAAGATAAG-----AAAGCTTAAGCAACAGAAAACTCTGAAACAGTCA 462  
Qy 242 ValValPheGlyGlyGluAlaArgLeuileThrGluLysGlnGluGluHisAsn 261  
Db 463 -----GATACGAAAGTAGATCTTAAGCAATATTGACAAAGAGCTTTAAT 504  
Qy 262 PhePheLeuAlaProGlyThrCysValValAspThrGlyileThrAsnSerGlnThrLeu 281  
Db 505 CATCAAAAAGTCAA-----GAACCGGATCATCAATGAAGAT----- 543  
Qy 282 IleProAspCysGlnLysLysTrpIleGlnSerileMetAspMetLeuGlnArgGlnGly 301  
Db 544 ---AAAGATTCTATGCTGAAAAAATCGAAGATATTCTGTAACAAAGCTCAACACAGAT 600  
Qy 302 LeuArgProileProGluAlaGluile-----GlyLeuAlaValIlePheMetThrThr 319  
Db 601 AAAAAAGAGATGCCGAAGTTAAGGTTCTGTAAGAACTAGGTAAACTCTTTAGTTCAACT 660  
Qy 320 LysAsnTyrCysAspPro-----GlnGlyHisProSerThrGlyLeuLysThrThrThr 337  
Db 661 AAAGCTGGTCTGATCAAGAAATTCAGAGCAT-----GTGAAGAAAGAAACG 708  
Qy 338 ProGlyProSerLeuSerGlnGlyValSerValAspGluLysLeuMetProSerAlaPro 357  
Db 709 AGTAGTGAGGAAAAATACTCAG-----AAAGTTGATGAACACTAT----- 747  
Qy 358 ValAsnThrThrThrValAlaAspThrGluSerGluGlnAlaAspThrTrpAspLeu 377  
Db 748 GCTAATAGGCTTTCAGAACCTTGCTCAAAAATCTCTTGAAGAACTAGTAAAGCAACTACC 807  
Qy 378 SerGluArgProLysGluileLysValSerLysMetGlu-----GlnLys----- 392  
Db 808 ATGAACAAGCTACACAGTTAAATCAATCTTTAGAAAACCGCTCAAAAGCTCAAGAA 867  
Qy 393 -----PheArgMetLeuSerGlnAspAla 400  
Db 868 ATCAACCTCTTATCAAGAAACGAATGTGAATTTGATAAGGCTATGAGTGAGAGCTTG 927  
Qy 401 ProThrValLysGluSerCysLysThrSerSerAsnAsnAsn-----SerMetValSer 418  
Db 928 GAGCAGGTTTGAAGGAATTTAAACATATAATTCGGAAGCTAATTTAGAAAGATTTGGTTGC 987  
Qy 419 AsnThrLeuAlaLysMetArgIleProAsnTyrGlnLeuSerProThrLys-----LeuPro 437  
Db 988 AAATCTAAAGAAATCGTAGAGAAATACGAAGGAAAACTTAATCAATCTAAATACTTCCA 1047  
Qy 438 SerIleAsnLysSerLysAspAlaSerGln-----GlnGlnGlnThrAsnSerIle 455

Db 1048 GAATTAAGCACTAGAGAGGAGCTCATTCGAAGTTGAAACAAGTTGTGGAGGATTTT 1107  
Qy 456 ArgAsnTyrPheGlnProSer-----ThrLysLysArgGluArgAsp--- 469  
Db 1108 AGAAAAAATTTAAACGTCAGAGCAAGTGCACCAAAAAACGCTCTCAACAGAGATTTA 1167  
Qy 470 -----GluGluAsnGlnGluMetSerSerCysLysSerAlaArgIleGluThrSer 486  
Db 1168 GCTGCTAATGAAATAATCAACA-----AGATTGATTAAACA 1206  
Qy 487 CysSerLeuLeuGluGlnThrGlnProAlaThrProSerLeuTrpLysAsnLysGluGln 506  
Db 1207 GTTTCA-----CCAGAGAATATCACTGTATATGAAGTGAAGCGTG 1248  
Qy 507 HisLeuSerGluAsnGluProValAspThrAsnSerAspAsnLeuPheThrAsp--- 525  
Db 1249 AAATTTACA-----GTCACAGCTAAAGTGAATTCGAAGCAGACGTTGGACTTC 1296  
Qy 526 ThrAspLeuLysSerIleValLysAsnSerAlaSerLysSerHisAlaAlaGluLysLeu 545  
Db 1297 AGTATCTT-----TTAACAAATAATATCCGCTCTGTATCA-----GATAGAATT 1341  
Qy 546 ArgSerAsnLysLysArgGluMetAspValAlaIleGluAspGluValLeuGluGln 565  
Db 1342 AGTACAATTTATAAGACTAACACGGATAATCATAAAGATTGCCGAATCACTATCAAGAAT 1401  
Qy 566 Leu-----PhelysAspThrLys----- 571  
Db 1402 TTGAAGCTAAATGAAGTCAACAGTCACTCTAAAGCTAAAGCTATTCGGCAATGTA 1461  
Qy 572 ProGluLeuGluIleAspValLysValGlnLysGlnGluAspValAsnValArgLys 591  
Db 1462 GTTGAAAAACATTCATTTACAGTGCAGAAAGAAAGAGGAGAA---CAAGTTCCTAAA 1518  
Qy 592 ArgProArgMetAspIleGluThrAsnAspThrPheSerAspGluAlaValProGluSer 611  
Db 1519 ACACCA-----GAGCAGAAAGATCTTAAACGGAAGAAAGAGTTCTCTCAAGAA 1566  
Qy 612 SerLysIleSerGlnGluAsnGluIle-----GlyLysLysArgGluLeu 626  
Db 1567 CCATAATCAAAATGACAGAAATCAATTAACAGAGTTGATTAAATCAGTCTCAACAGAACTG 1626  
Qy 627 Lys----- 627  
Db 1627 GAAAGTTAGAAAAGCAATAAAGAAATTATGGAGCAACAGAGATTCATCCATCCA 1686  
Qy 628 -----GluAspSerLeuTrp---SerAlaLysGlu-----Ile 637  
Db 1687 GAGTATGCTATTCAAAATCTATTGGAGTCACAAAAAGAGCCTATCCAGAGGCCATA 1746  
Qy 638 SerAsnAsnAspLysLeuGlnAspSer----- 647  
Db 1747 ACAAGTTTAAAGAGATTATTGGTGAATTCATCTTCAAAATACTACACAGACACTATTTT 1806  
Qy 648 -----GluMetLeuPro 651  
Db 1807 AACAAATATAATCTCATTTTATGAAATTATCAACTTCATGCAACAATGGAGATGCTGACT 1866  
Qy 652 LysLysLeuLeuLeu-----ThrGluPheArgSerLeuVal 663  
Db 1867 AGAAAGTGGTTTCAGTATATGAACAAATATCTGTATAATGCAGAAATTAATAAG---ATA 1923  
Qy 664 IleLysAsnSerThrSerArgAsnProSerGlyIleAsnAspAspTyrGlyGlnLys 683  
Db 1924 TTTGAGTCAGATATGAAGAGAACGAAA-----GAAGATAATTACGGAAGTTTAGAA 1974  
Qy 684 Asn-----PhelysLysPhe----- 688  
Db 1975 AATGATGCTTTGAAAGGCTATTTTGAGAAATATTTCTTACACCATTTAATAAAATTAAG 2034  
Qy 689 -----LysLysValThrTyrProGlyAlaGlyLysLeuProHis 701

Db 2035 CAGATTGTAGATGATTTTCGATAAAAAAGTAGAACCAAGATCAGCCAGCAACCAATTCGGAA 2094  
Qy 702 IleIleGlyGlySerAspLeuIleAlaHisHisAlaArgLysAsnThrGluLeuGluGlu 721  
Db 2095 -----AATTGCAATGATCAGGTAAGGAAAGCTTAAGATTGCTGTATCGAAG 2145  
Qy 722 TrpLeuArgGlnGluMetGluValGlnAsnGlnHis-----AlaLysGluGluSerLeu 739  
Db 2146 TATATGAGTAAGGTTTATGATGAGTTTCATCAACATCTCAGAAGAAAAATCACAGTAAA 2205  
Qy 740 AlaAspAspLeuPheArgTyrAsnProTyrLeuLysArgArg 753  
Db 2206 ATTGTGATCTTTTAAAGGAACCTTGAAGCGATTAAACAACA 2247  
RESULT 13  
US-09-214-564A-5  
; Sequence 5, Application US/09214564A  
; Patent No. 6150515  
; GENERAL INFORMATION:  
; APPLICANT: Sharp, Phillip A.  
; TITLE OF INVENTION: Tat-SR: Cofactor For Stimulation Of Transcriptional  
; ; Elongation By HIV-1 Tat  
; FILE REFERENCE: M0656/7042  
; CURRENT APPLICATION NUMBER: US/09/214,564A  
; CURRENT FILING DATE: 1999-08-18  
; PRIOR APPLICATION NUMBER: US 60/021,218  
; PRIOR FILING DATE: 1996-07-03  
; PRIOR APPLICATION NUMBER: US 60/033,152  
; PRIOR FILING DATE: 1996-12-13  
; PRIOR APPLICATION NUMBER: PCT/US97/11713  
; PRIOR FILING DATE: 1997-07-03  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 2672  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 58..2319  
US-09-214-564A-5  
Alignment Scores:  
Pred. No.: 1.08e-06 Length: 2672  
Score: 157.50 Matches: 138  
Percent Similarity: 31.92% Conservative: 95  
Best Local Similarity: 18.90% Mismatches: 259  
Query Match: 4.04% Indels: 238  
DB: 3 Gaps: 29  
US-09-837-602-2 (1-754) x US-09-214-564A-5 (1-2672)  
Qy 59 GlnThrAspGluIleProValLeuThrLeuLysAspAsnSerLysTyrGlyThr----- 76  
Db 547 CACACAGAGAAATTTAAGGTCAAACTTTTACAAAGATAATCAA-----GGAAATCTTTAAA 600  
Qy 77 -----PheValAsnGluGluLysMetGlnAsnGlyPheSerArgThr 90  
Db 601 GGAGACGGTCTTGTCTGTTTATTGAAAAGAGATCTGTGGAA-----CTTGCA 648  
Qy 91 LeuLysSerGlyAsp-----GlyIleThrPheGlyValPheGlySerLys 105  
Db 649 TTAATACTTTTGGATGAAGATGAAATTTAGAGGCTTACAAATTACATGTTGAGTGGCAAG 708  
Qy 106 PheArgIle-----GluTyrGluProLeuValAlaCysSerSerCysLeuAspValSer 123  
Db 709 TTTCACTGAAGGAGAAATATGATGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 768  
Qy 124 GlyLysThrAlaLeuAsnGlnAlaIleLeuGlnLeuGlyGlyPheThrValAsnAsnTrp 143  
Db 769 AAGAGCTGTCTATGCAACAAAGACAGTTG-----GATTGG 804

Qy	144	ThrGluGlu     	-----CysThrHis     	-----	149
Db	805	AGACCTGAGCGCGAGCGGACCATCCGGATGCCCATGCGGAGTTGTTCATCATCAAG		864	
Qy	150	-----	--LeuValMetValSerVallylsVal       	157	
Db	865	AATATGTTTTCATCTCTAATGGATTTTGAGGATGATCCGGTGTGTCTGAATGAGATCAGAGAA		924	
Qy	158	ThrIleLysThrIleCysAlaLeuLeuCysGlyArgProIleVallylsProGluTyPhe : : : : :     : : :     : : :		177	
Db	925	GACCTTCGAGTAGAGTCTCG	-----AAGTYT	951	
Qy	178	ThrGluPheLeuLysAlaValGlnSerLysLysGlnProProGlnIleGlu	-----Ser	195	
Db	952	GGACAAATAAGGAAACTCTCTCTCTTTGATAGGCACCCAGATGCTGTGGCTCTGTGTGCC	: : : : :     : : :     : : :	1011	
Qy	196	PheTyrrProLeuAspGluProSerIleGlySerLysAsnValAsp	-----Leu	212	
Db	1012	TTTCGGGATCCA---GAGGAAGCTGATTATTGTATTTCAGACTCTCGATGGAAGATGGTTT	: : : : :     : : :     : : :	1068	
Qy	213	SerGlyArgGlnGluArGLysGlnIlePheLysGlyLysThrPheIlePheLeuAsnAla	232		
Db	1069	GGTGGCGCTCAAATCACTGCCCGCATGGATGGACTACA	-----	1110	
Qy	233	LysGlnHisLysLysLeuSerSerAlaValPheGlyGlyGluAlaArgLeuIle	252		
Db	1111	-----	-GATTATCAGGTGGAGGAAACC	1131	
Qy	253	ThrGluGluAsnGluGluGluHisAsnPhePheLeuAlaProGlyThrCysValValAsp	272		
Db	1132	TCAAGAGAAGGAGGAGGAAGG	-----	1152	
Qy	273	ThrGlyIleThrAsnSerGlnThrLeuIleProAspCysGlnLysLysTrpIleGlnSer	292		
Db	1153	-----	-CTGAGAGATCG	1164	
Qy	293	IleMetAspMetLeuGlnArgGlnGlyLeuArgProIleProGluAlaGluIleGlyLeu	312		
Db	1165	-----	-GAGGCTTCTCTCAATGCTCTCGAGGCCAACAGAGGCCTT	1203	
Qy	313	AlaValIlePheMetThrThrLysAsnTyrcysAspPro	-----Gln	326	
Db	1204	AGCGTTTCAGATTCTGCTCTCTCTCGAAAGCGAGCGCTTCTAGACGAGGCATTTTTTCA	1263		
Qy	327	GlyHisProSerThrGly	-----	332	
Db	1264	GAGCACCCCAGCACATCTAAATGAATGCTCAAGAAACTGCAACTGGAATGGCATTTGAA	1323		
Qy	333	-----	--LeuLysThrThrThrProGlyProSerLeuSerGlnGly	345	
Db	1324	GAACCTTAGATGAGAAGAGTTTGAAGACAGACAGATGGGGAGAAATTTGAAGAAGGT	1383		
Qy	346	ValSerValAspGluLysLeuMetProSerAlaProValAsnThrThrThrTyrrValAla	365		
Db	1384	GCTTCTGAACAACATGCTTAAGGAAGTAGCCCCGAAAAAGAGGCGTGAAGAAGCGCTGCCCT	1443		
Qy	366	AspThrGluSerGluGlnAlaAspThrTrpAspLeuSerGluArgProLysGluIleLys	385		
Db	1444	GA AAAAGAAATCTGAAGAGGCG	-----TGCCCCAAAAGAGGGTTTGAAGGCAGC	1491	
Qy	386	ValSerLysMetGluGlnLys	-----PheArgMetLeuSerGlnAspAlaPro	401	
Db	1492	TGCTCCCAAAAAGAGTCTGAAGAAGGCCAATCCCGTAAGAGGATCTGAAGAGGATAGTCTCT	1551		
Qy	402	ThrValLysGluSerCysLysThrSerSerAsnAsnSerMetValSerAsnThrLeu	421		
Db	1552	-----AAAAAAGAGTCTTAAAAAAGAACACACTCAAAAATGATTGTGAAGAGAATGGCCTT	1605		
Qy	422	AlaLys	-----MetArgIleProAsnTyrrGlnLeuSerProThrLys	435	
Db	1606	GCAAGGNAATCGAAGATGACCTCAACAGGAGTGCTGAAGAGGAGGTTGGCCCCACAAA	1665		
Qy	436	Leu	-----ProSerIleAsnLysSerLysAspArgAlaSerGlnGlnGln	451	

1666 GAGTCCGAGAAGATGACTCAGAGAAAGAGCTGTGATCAGAGACTGCTCTGAAAAACAGTCT 1725  
452 ThrAsnSerIleArgAsnTyrPheGlnProSerThrLysLysArgGluArgAspGluGlu 471  
1726 GAAGATGGCTCCGAAGAAGAAATTGGAAGAAATGGTCTCGAAGAAAGATTGGACGAGGAA 1785  
472 AsnGlnGluMetSerSerCysLysSerAlaArgIleGluThrSerCysSerLeuLeuGlu 491  
1786 GGTTCCTCAA----- 1794  
492 GlnThrGlnProAlaThrProSerLeuTyrLysAsnLysGluGlnHisLeuSerGluAsn 511  
1795 -----AAGAGAGCTTCATGAAAATGTTCTTGACAAA 1824  
512 GluProValAspThrAsnSerAspAsnAsnLeuPheThrAspThrAspLeuLysSerIle 531  
1825 GAGTTAGAAGAAATGACTCTGAAATCTCGAAATTTGAAGATGACGGCTCTGAAAAGTG 1884  
532 ValLysAsnSerAlaSerLysSerHisAlaAlaGluLysLeuArgSerAsnLysLysArg 551  
1885 TTAGATCAGGAAGGCTCTGAGAGAGAGATTTCACGAAGAT-----TCAGATGAAAAGGAA 1938  
552 GluMetAspAspValAlaIleGluAspGluValLeuGluGlnLeuPheLysAspThrLys 571  
1939 GAA-----GAGGAGGATACATATCAAAAAGTATTTCATGATGATGATCT 1980  
572 ProGluLeuGluIleAspValLysGlnGlnLysGlnGluAspValAsnValArgLys 591  
1981 GATGAGAAAGAG-----GATGAAGATATGCAGATGAAAAGGGG 2019  
592 ArgProArgMetAspIleGluThrAsnAspThrPheSerAspGluAlaVal---ProGlu 610  
2020 CTTGAAGCTGCTGATAAAAGCGGAGAGAGGTGATGCAGATGAAAAGCTGTTTGAAGAG 2079  
611 SerSerLysIleSerGlnGluAsnGluIleGlyLysLysArgGluLeuLysGluAspSer 630  
2080 TCAGATGACAAGGAAGATGAAGATGCAGATGGAAGGAAGAGTTGAAGATGCTGACGAAAAG 2139  
631 LeuTrpSerAlaLysGluIleSerAsnAsnAspLysLeuGlnAspAspSerGluMetLeu 650  
2140 TTGTTC-----GAAGATGATGATTTCCATGAGAAGTTGTTGATGAGGAGGAAGATTCC 2193  
651 ProLysLysLeuLeuLeuThrGluPheArgSerLeuValIleLysAsnSerThrSerArg 670  
2194 AGTGAGAGTTGTT----- 2208  
671 AsnProSerGlyIleAsnAspTyrGlyGlnLeuLysAsnPheLysLys-PhelLys 690  
2209 -----GACGATTCTGATGAGGGGACTTTGGTGTTTGGAGTGTGAAGAA 2259  
690 sValThrTyrProGlyAlaGlyLysLeu 699  
2260 GGGCCCTATCCACTGCGCAGAGCTTTA 2287  
  
RESULT 14  
US-09-214-564A-1  
; Sequence 1, Application US/09214564A  
; Patent No. 6150515  
; GENERAL INFORMATION:  
; APPLICANT: Sharp, Phillip A.  
; APPLICANT: Zhou, Qiang  
; TITLE OF INVENTION: TAT-SF: Cofactor For Stimulation Of Transcriptional  
; TITLE OF INVENTION: Elongation By HIV-1 TAT  
; FILE REFERENCE: M0656/7042  
; CURRENT APPLICATION NUMBER: US/09/214,564A  
; CURRENT FILING DATE: 1999-08-18  
; PRIOR APPLICATION NUMBER: US 60/021,218  
; PRIOR FILING DATE: 1996-07-03  
; PRIOR APPLICATION NUMBER: US 60/033,152  
; PRIOR FILING DATE: 1996-12-13  
; PRIOR APPLICATION NUMBER: PCT/US97/11713  
; PRIOR FILING DATE: 1997-07-03

```

; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2815
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 110..2371
; NAME/KEY: unsure
; LOCATION: 46..46
; OTHER INFORMATION: n = a, c, g or t
; NAME/KEY: unsure
; LOCATION: 2731..2731
; OTHER INFORMATION: n = a, c, g or t
; US-09-214-564A-1

Alignment Scores:
Pred. No.: 1.18e-06 Length: 2815
Score: 157.50 Matches: 138
Percent Similarity: 31.92% Conservative: 95
Best Local Similarity: 18.90% Mismatches: 259
Query Match: 4.04% Indels: 238
DB: 3 Gaps: 29

US-09-837-602-2 (1-754) x US-09-214-564A-1 (1-2815)

Qy 59 GlnThrAspGluLeuProValLeuThrLeuLysAspSerLysTyrGlyThr----- 76
Dy 599 CAGACAGAGAATTTAAGGCTCAAACTTTACAAAGATAATCAA-----GGAAATCTTAAA 652
Qy 77 -----PheValAsnGluGluLysMetGlnAsnGlyPheSerArgThr 90
Dy 653 GGACACGGCTTCTGCTTATTGCAAAAGAAATCTGTGNA-----CTTGCA 700
Qy 91 LeuLysSerGlyAsp-----GlyLeuThrPheGlyValPheGlySerLys 105
Dy 701 TTAATACTTTTGGATGAAGATGAATTAGAGGCTACAAATTTACATGTTGAGGTGGCAAG 760
Qy 106 PheArgLeu-----GluTyrGluProLeuValAlaCysSerSerCysLeuAspValSer 123
Dy 761 TTTCACTGAAGGAGGAATATGATGCTCTCAAGAGAGAAAGAAAGACTATAAG 820
Qy 124 GlyLysThrAlaLeuAsnGlnAlaLeuGlnLeuGlyGlyPheThrValAsnAsnTyr 143
Dy 821 AAGAGCTGCTGTGCAACAAAGCAGTTG-----GATTGG 856
Qy 144 ThrGluGlu-----CysThrHis----- 149
Dy 857 AGACCTGAGAGCGAGCGGACCATCCGGATGCGCATGAGCGAGTTGTTCATCATCAAG 916
Qy 150 -----LeuValMetValSerValLysVal 157
Dy 917 AATATGTTTCATCTATGATTTTGGAGATGATCCGTTGGTGTGTAATGATGATGAGAGAA 976
Qy 158 ThrIleLysThrIleCysAlaLeuIleCysGlyArgProIleValLysProGluTyrPhe 177
Dy 977 GACCTTCGAGTAGAGTTGCG-----AAGTTT 1003
Qy 178 ThrGluPheLeuLysAlaValGlnSerLysLysGlnProGlnIleGlu-----Ser 195
Dy 1004 GGACAAATTAGGAAACTCTCTCTTTGATAGGACCCAGATGTTGTTGGCTCTGTGTCTC 1063
Qy 196 PheTyrProProLeuAspGluProSerIleGlySerLysAsnValAsp-----Leu 212
Dy 1064 TTTCCGGATCCA---GAGGAGCTGATGATTTGTTATTCAGACTCTCGATGGAGATGGTTT 1120
Qy 213 SerGlyArgGlnGluArgLysGlnIlePheLysGlyLysThrPheIlePheLeuAsnAla 232
Dy 1121 GGTGGCCGTCAATCACTGCTCCAGGCGATGGATGGGACTACA----- 1162
Qy 233 LysGlnHisLysLysLeuSerSerAlaValValPheGlyGlyGlyGluAlaArgLeuIle 252
;

```

```

1163 -----GATTATCAGGTGGAGGAAACC 1183
Qy 253 ThrGluGluAsnGluGluGluHisAsnPhePheLeuAlaProGlyThrCysValValAsp 272
Dy 1184 TCAAGAGAAGGGAGGAAGG----- 1204
Qy 273 ThrGlyIleThrAsnSerGlnThrLeuIleProAspCysGlnLysLysThrIleGlnSer 292
Dy 1205 -----CTGAGAGGATGG----- 1216
Qy 293 IleMetAspMetLeuGlnArgGlnGlyLeuArgProIleProGluAlaGluIleGlyLeu 312
Dy 1217 -----GAGGCTTTCTCAATGCTCTGAGGCCAACAGAGGCTTT 1255
Qy 313 AlaValIlePheMetThrThrLysAsnTyrCysAspPro-----Gln 326
Dy 1256 AGCGTTCAAGATTCGTCTCTGCTTCGAAAGGCGAGGCTTCTAGACGAGGCAATTTTCA 1315
Qy 327 GlyHisProSerThrGly----- 332
Dy 1316 GAGCACCCCGACACATCTAAATGAATGCTCAAGAAACTGCAACTGGAATGGCATTTGAA 1375
Qy 333 -----LeuLysThrThrThrProGlyProSerLeuSerGlnGly 345
Dy 1376 GAACCTATAGATGAGAAGAGAGTTTGAAGAACACAGAGATGGGGAGAAATTTGAAGAGGT 1435
Qy 346 ValSerValAspGluLysLeuMetProSerAlaProValAsnThrThrThrTyValAla 365
Dy 1436 GCTTCTGAAACAACTCTAAGGAAAGTAGCCCGGAAAGAGAGCTGAAGAGGCTGCCT 1495
Qy 366 AspThrGluSerGluGlnAlaAspThrTrpAspLeuSerGluArgProLysGluIleLys 385
Dy 1496 GAAAGAGATCTCAAGAGGCG-----TGCCCCAAAGAGGGTTTGAAGGCGAGC 1543
Qy 386 ValSerLysMetGluGlnLys-----PheArgMetLeuSerGlnAspAlaPro 401
Dy 1544 TGCTCCCAAAAGAGCTCTGAAGAGGCAATCCCGTAAGAGAGTCTGAAGAGGATAGTCT 1603
Qy 402 ThrValLysGluSerCysLysThrSerSerAsnAsnSerMetValSerAsnThrLeu 421
Dy 1604 -----AAAAAGAGTCTAAAAAGACACACTCAAAATGATTTGTGAGAGATGGCTT 1657
Qy 422 AlaLys-----MetArgIleProAsnTyrGlnLeuSerProThrLys 435
Dy 1658 GCAAGAGATCTGAAGATGACCTCAACAAGAGTCTGAAGAGGAGGTGGCCCCACAAA 1717
Qy 436 Leu-----ProSerIleAsnLysSerLysAspArgAlaSerGlnGlnGln 451
Dy 1718 GAGTCCGAGAGAGATGACTCAGAGAAAGAGTCTGATGAAGAGCTGCTCTGAAACAGTCT 1777
Qy 452 ThrAsnSerIleArgAsnTyrPheGlnProSerThrLysLysArgGluArgAspGluGlu 471
Dy 1778 GAAGATGGCTCCGAAAGAGAAATTTGAAGAAATGGTCTCGAGAAAGATTTGGACGAGAA 1837
Qy 472 AsnGlnGluMetSerSerCysLysSerAlaArgIleGluThrSerCysSerLeuLeuGlu 491
Dy 1838 GGTCTCTGAA----- 1846
Qy 492 GlnThrGlnProAlaThrProSerLeuTrpLysAsnLysGluGlnHisLeuSerGluAsn 511
Dy 1847 -----AAGAGCTTCATGAAATGTTCTTGACAAA 1876
Qy 512 GluProValAspThrAsnSerAspAsnAsnLeuPheThrAspThrAspLeuLysSerIle 531
Dy 1877 GAGTTAGAGAAATGACTCTGAAACTCCGAATTTGAAGATGACGCTCTGAAAAAGTG 1936
Qy 532 ValLysAsnSerAlaSerLysSerHisAlaAlaGluLysLeuArgSerAsnLysLysArg 551
Dy 1937 TTATGATGAGGAGGCTCTGAGAGAGAGTTTGAACCAAGAT-----TCAGATGAAAGGAA 1990
Qy 552 GluMetAspValAlaIleGluAspGluValLeuGluGlnLeuPheLysAspThrLys 571
Dy 1991 GAA-----GAGGAGGATACATATGAAAGAGTATTGTATGATGAGTCT 2032

```



Qy 572 ProGluLeuGluLeuAspValIysValGlnIysGlnGluAspValAsnValArgIys 591  
Dy 2033 GATGAGAAAGAG- - - - -GATGAAGAATATGCAGATGAAGAAGGG 2071  
Qy 592 ArgProArgMetAspIleGluThrAsnAspThrPheSerAspGluAlaVal- - -ProGlu 610  
Dy 2072 CTTGAGCTGCTGATAAAGCGGAGAGAGGTGATGCAGATGAAGAAGCTTTTGAAGAG 2131  
Qy 611 SerSerIysIleSerGlnGluAsnGluLeuGlyIysIysArgGluLeuLysGluAspSer 630  
Dy 2132 TCAGATCAAGGAAGATGAAGATGCAGATGGAAGAAGTGAAGATGCTGACGAAAG 2191  
Qy 631 LeuTrpSerAlaLysGluIleSerAsnAsnAspIysLeuGlnAspSerGluMetLeu 650  
Dy 2192 TTGTTC- - - - -GAAGATGATGATTCGAATGAGAAGTTGTTTGTGATGAGGAGAGATTCC 2245  
Qy 651 ProLysIysLeuLeuLeuThrGluPheArgSerLeuValIleLysAsnSerThrSerArg 670  
Dy 2246 AGTGAGAAGTTGTT- - - - - 2260  
Qy 671 AsnProSerGlyIleAsnAspAspIysGlnLeuLysAsnPheLysLys- PheLysLY 690  
Dy 2261 - - - - -GACGATCTGATGAGAGGGGACTTTGGTGGTGTGAGTGTGAAGAA 2311  
Qy 690 sValThrTyrProGlyAlaGlyLysLeu 699  
Dy 2312 GGGCCCTATCCACTGCGCAGCAGCTTTA 2339

## RESULT 15

US-08-242-932-1

Sequence 1, Application US/08242932

Patent No. 5595740

GENERAL INFORMATION:

APPLICANT: Brady, L. Jeannine

TITLE OF INVENTION: Cloning of No. 5595740-IgA Fc Binding Forms of

TITLE OF INVENTION: the Group B Streptococcal Beta Antigens

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik &amp; Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: FL

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/242,932

FILING DATE: 16-MAY-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Saliwanchik, David R.

REGISTRATION NUMBER: 31,794

REFERENCE/DOCKET NUMBER: UF142

TELECOMMUNICATION INFORMATION:

TELEPHONE: 904-375-8100

TELEFAX: 904-372-5800

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4200 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-242-932-1

Alignment Scores:

Pred. No.:

Score:

2.63e-06

Length:

157.00

Matches:

4200

144

Percent Similarity: 36.96% Conservative: 121  
Best Local Similarity: 20.08% Mismatches: 236  
Query Match: 4.03% Indels: 216  
DB: 1 Gaps: 40

US-09-837-602-2 (1-754) x US-08-242-932-1 (1-4200)

Qy 192 GlnIleGluSerPheTyrProProLeuAspGluProSerIleGlySerLysAsnValAsp 211  
Dy 710 CAGAAAAATGAGTTTAAACCAAAATTTGATGAAACAAATGATCTTGATGCTATTAGAA 769  
Qy 212 LeuSerGlyArg- - - - -GlnGluArgLysGlnIle 221  
Dy 770 TTAGAAAAATCAATTTAACGAAACTTAATAGACTGTTCACACATCAACAAACATGAAGAAGTT 829  
Qy 222 PheLysGlyLysThrPheIlePheLeuAsnAlaLysGlnHisLysLysLeuSerSerAla 241  
Dy 830 GAGAAAGATAG- - - - -AAAGCTTAAGCAACAGAAAACCTCTGAAACACTCA 874  
Qy 242 - - - - -ValValPheGlyGlyGluAlaArgLeuIleThrGluGluAsnGluGlu 258  
Dy 875 GATACGAAAGCTAGATCTTAAGCAATATTGACAAAGAGCTTAATCATCAAAAAAGCTCAAGTT 934  
Qy 259 GluHisAsnPhePheLeuAlaProGlyThrCysValValAspThrGlyIleThrAsnSer 278  
Dy 935 GAA- - - - -AAAATGCGAGAGCAAAAGGGAATCACAATGAA 970  
Qy 279 GlnThrLeuIleProAspCysGlnLysLysThrIleGlnSerIleMetAspMetLeuGln 298  
Dy 971 GAT- - - - -AAAGATTCTTGTGTAAGAAAATCGAAGATATTCTGTAACAAAGCTCAA 1031  
Qy 299 ArgGlnGlyLeuArgProIleProGluAlaGluIle- - - - -GlyLeuAlaValIlePhe 316  
Dy 1022 CAACGAGATAAAAGAGAGATGCCGAAGTAAAGGTCGTGAAGAACTAGGTAACTCTTT 1081  
Qy 317 MetThrThrLysAsnTyrCysAspPro- - - - -GlnGlyHisProSerThrGlyLeuLys 334  
Dy 1082 AGTTCAACTAAAGCTGCTGATCAAGAAATTCAGAGCAT- - - - -GTCAAG 1129  
Qy 335 ThrThrThrProGlyProSerLeuSerGlnGlyValSerValAspGluLysLeuMetPro 354  
Dy 1130 AAAGAAACGAGTAGTGAGGAAAATACTCAG- - - - -AAAGTTGATGAACACTAT- 1177  
Qy 355 SerAlaProValAsnThrThrTyrValAlaAspThrGluSerGluGlnAlaAspThr 374  
Dy 1178 - - - - -GCTAATAGCCTTCAGACCTTGCTCAAAAATCTCTTGAAGAACTAGATAAG 1228  
Qy 375 TrpAspLeuSerGluArgProLysGluIleLysValSerLysMetGlu- - - - -GlnLys 392  
Dy 1229 GCAACTACCAATGAACAAGCTACACAAGTTAAAAATCAATTTCTAGAAAAACGCTCAAAAG 1288  
Qy 393 - - - - -PheArgMetLeuSer 397  
Dy 1289 CTCAAAGAAATACAACTCTTATCAAGAAACGAATGTGAATTTGTAAGGCTGATAGT 1348  
Qy 398 GlnAspAlaProThrValLysGluSerCysLysThrSerSerAsnAsnAsn- - - - -Ser 415  
Dy 1349 GAGAGCTTGGAGCAGGTTGAGAGGAAATTAACATAATTCGGAAGCTAATTTAGAAGAT 1408  
Qy 416 MetValSerAsnThrLeuAlaLysMetArgIleProAsnTyrGlnLeuSerProThrLys 435  
Dy 1409 TTGTTGCGAAATCTAAAGAAATCGTAAGAGATACGAAGGAAACCTTAATCAATCTAAA 1468  
Qy 436 - - - - -LeuProSerIleAsnLysSerLysAspArgAlaSerGln- - - - -GlnGlnGlnThr 452  
Dy 1469 AATCTTCCAGATTAAGACCACTAGAGAGAGAGCTCATTCGAAGTTGAAACAAAGTTGTG 1528  
Qy 453 AsnSerIleArgAsnTyrPhe- - - - -GlnProSerThrLysLysArg- - - - -Glu 467  
Dy 1529 GAGGATTTAGAAAAAATTTAAACGCTCAGACAGTGACACCAAAAAACGCTGTCAAA 1588  
Qy 468 ArgAsp- - - - -GluGluAsnGlnGlnMetSerSerCysLysSerAlaArgIle 483

```
Db 1589 CGAGATTAGCTGCTAATAAGAAATAATCAACAA-----AGATT 1627
Qy 484 GluThrSerCysSerLeuLeuGluGlnThrGlnProAlaThrProSerLeuTrpLysAsn 503
Db 1628 GAGTTAACAGTTTCA-----CCAGAGATATCACTGTATATGAAGGT 1669
Qy 504 LysGluGlnHisLeuSerGluAsnGluProValAspThrAsnSerAspAsnLeuPhe 523
Db 1670 GAGACGTGAAATTTACA-----GTCACAGCTAAAGCTGATTCGAAGCAGC 1717
Qy 524 ThrAsp---ThrAspLeuLysSerIleValIleAsnSerAlaSerLysSerHisAla 542
Db 1718 TTGCACTTCAGTGATCTT-----TTAACAAATATATATCCGTCTGTATCA----- 1762
Qy 543 GluLysLeuArgSerAsnLysLysArgGluMetAspValAlaIleGluAspGluVal 562
Db 1763 GATAGAATTAGTACAAATTATAGACTTAACACGGATTAATCATAAGATTGCCGAAATCACT 1822
Qy 563 LeuGluGlnLeu-----PheLysAspThrLys 571
Db 1823 ATCAAGAATTGTGAAGCTAAATGAAAGTCAACACAGTGACTCTAAAGAGCTAAAGATGATTCT 1882
Qy 572 -----ProGluLeuGluIleAspValIleAspValIleGlnLysGlnGluAspValAsn 588
Db 1883 GGCAATGTAGTTGAAAGAAACAACTTCACTATTACAGTCAAAAGAAAGAGAGAGAA---CAA 1939
Qy 589 ValArgLysArgProArgMetAspIleGluThrAsnAspThrPheSerAspGluAlaVal 608
Db 1940 GTTCTTAACACCA-----GAGCAGAAAGATTCTAAACCGGAAGAAAGGTT 1987
Qy 609 ProGluSerSerLysIleSerGlnGluAsnGluIle-----GlyLysLys 623
Db 1988 CCTCAAGAACCAAAATCAAAATGACAAGATCAATTACAAGAGTTGATTAAATCAGCTCAA 2047
Qy 624 ArgGluLeuLys----- 627
Db 2048 CAAGAAGCTGGAAAGATTAGAAAAAGCAATAAAGAAATTAATGGAGCAACAGAGATTCCA 2107
Qy 628 -----GluAspSerLeuTrp---SerAlaLysGlu----- 636
Db 2108 TCCAAATCCAGAGATATGTTTCAAAATCTATTTTGGGAGTCACAAAAGAGCCTATCCAG 2167
Qy 637 -----IleSerAsnAsnAspLysLeuGlnAspAspSer----- 647
Db 2168 GAAGCCATAACAAGTTTAAAGAGATTATTGGTGATTCTCTTCAAAATACTACACAGAG 2227
Qy 648 -----Glu 648
Db 2228 CACTATTTTAACAAATAATAATCTGATTTTATGAATTAATCAACTTCATGCACAAATGGAG 2287
Qy 649 MetLeuProLysLysLeuLeu-----ThrGluPheArg 660
Db 2288 ATGCTGACTAGAAAGTGTTTCAGTATATGAAACAAATATCTCTGATATGCGAATAATTAA 2347
Qy 661 SerLeuValIleLysAsnSerThrSerArgAsnProSerGlyIleAsnAspAspTyrGly 680
Db 2348 AAG---ATATTTGAGTCAGATATGAAGAGACGAAA-----GAAGATAATTACGGA 2395
Qy 681 GlnLeuLysAsn-----PheLysLysPhe----- 688
Db 2396 AGTTTAGAAAATGATGCTTTGAAAGGCTATTTTGGAGAAATATTTCTTACACCAATTTAAT 2455
Qy 689 -----LysLysValThrTyrProGlyAlaGlyLys 698
Db 2456 AAAATTAGCAGATTGTAGATTGTTGGATAAAAAAGTAGAACAAAGATCAGCCAGCACCA 2515
Qy 699 LeuProHisIleIleGlyGlySerAspLeuIleAlaHisHisAlaArgLysAsnThrGlu 718
Db 2516 ATTCGGAA-----AATTCAGAAATGATCAGGCTAAGGAAAGGCTAAGATTGCT 2566
Qy 719 LeuGluGluTrpLeuArgGlnGluMetGluValGlnAsnGlnHis-----AlaLysGlu 736
Db 2567 GTATCGAAGTATATGAGTAAAGGTTTATGAGTGGAGTTTCAACATCTGCAGAGAAAAAAT 2626
```

```
Qy 737 GluSerLeuAlaAspAspLeuPheArgTyrAsnProTyrLeuLysArgArg 753
Db 2627 AACAGTAAAAATTGTTGATCTTTTAAAGGAACTTGAAGCGATTAAACAACAA 2677
```

Search completed: January 6, 2004, 14:55:53  
Job time : 220 secs

BEST AVAILABLE COPY

BEST AVAILABLE COPY

BEST AVAILABLE COPY

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 6, 2004, 10:38:54 ; Search time 1312 Seconds  
(without alignments)

11615.852 Million cell updates/sec

Title: US-09-837-602-1

Perfect score: 4403

Sequence: 1 ttccgcacgagcgcggttg.....accgcggtgagctccagct 4403

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2263443 seqs, 1730637950 residues

Total number of hits satisfying chosen parameters: 4526886

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications NA:\*
- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
  - 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
  - 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
  - 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
  - 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
  - 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*
  - 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
  - 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
  - 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*
  - 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
  - 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*
  - 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
  - 13: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*
  - 14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*
  - 15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
  - 16: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
  - 17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
  - 18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	552.2	12.5	646	9	US-09-922-217-343
C 2	552.2	12.5	646	10	US-09-833-263-343
C 3	552.2	12.5	646	14	US-10-025-380-343
4	537.4	12.2	541	10	US-09-878-178-1737
5	537.4	12.2	541	14	US-10-046-935-1737
6	537.4	12.2	541	15	US-10-146-502-1737
7	507	11.5	587	15	US-10-102-524-532
8	405.6	9.2	468	11	US-09-918-995-13834
9	258.4	5.9	360	10	US-09-783-590-3449
10	239.4	5.4	272	9	US-09-923-876-5167
11	239.4	5.4	272	12	US-09-923-876-5167
C 12	212.6	4.8	475	10	US-09-917-800A-803
13	191	4.3	404	10	US-09-783-590-8929
14	167.6	3.8	315	10	US-09-960-352-8727
15	119.4	2.7	442	9	US-09-864-761-11287

16	114	2.6	114	9	US-09-864-761-27987	Sequence 27987, A
17	97.6	2.2	6237	13	US-10-311-455-331	Sequence 331, App
C 18	92.4	2.1	6237	13	US-10-311-455-332	Sequence 332, App
C 19	73.6	1.7	539	15	US-10-198-846-1369	Sequence 1369, Ap
20	72	1.6	9539	13	US-10-240-453-54	Sequence 54, Appl
21	72	1.6	9539	15	US-10-239-676-52	Sequence 52, Appl
C 22	71	1.6	14006	13	US-10-311-455-1931	Sequence 1931, Ap
C 23	70	1.6	6056	13	US-10-311-455-753	Sequence 753, App
24	69.6	1.6	15548	13	US-10-311-455-2128	Sequence 2128, Ap
25	69.6	1.6	3673778	13	US-10-312-841-1	Sequence 1, Appli
26	69.6	1.6	3673778	13	US-10-312-841-2	Sequence 2, Appli
C 27	69.2	1.6	2787	11	US-09-764-891-8349	Sequence 8349, Ap
C 28	69.2	1.6	2787	15	US-10-205-428-782	Sequence 782, App
29	68.2	1.5	6171	13	US-10-311-455-761	Sequence 761, App
30	68.2	1.5	6668	13	US-10-311-455-1670	Sequence 1670, Ap
31	68.2	1.5	8392	13	US-10-311-455-1463	Sequence 1463, Ap
32	67.2	1.5	446	10	US-09-960-352-3400	Sequence 3400, Ap
33	67	1.5	6145	13	US-10-311-455-945	Sequence 945, App
34	66.8	1.5	27007	10	US-09-764-868-1424	Sequence 1424, Ap
35	66.6	1.5	529	10	US-09-983-965-2109	Sequence 2109, Ap
36	66.2	1.5	17594	13	US-10-311-455-1999	Sequence 1999, Ap
37	65.8	1.5	6631	13	US-10-240-453-214	Sequence 214, App
C 38	65.8	1.5	6668	13	US-10-311-455-1670	Sequence 1670, Ap
39	65.2	1.5	6668	13	US-10-311-455-1669	Sequence 1669, Ap
C 40	65	1.5	8392	13	US-10-311-455-1463	Sequence 1463, Ap
C 41	64.4	1.5	3673778	13	US-10-312-841-2	Sequence 2, Appli
42	64	1.5	5291	13	US-10-311-455-1292	Sequence 1292, Ap
43	64	1.5	5291	13	US-10-240-453-58	Sequence 58, Appl
44	64	1.5	8417	12	US-10-074-024-635	Sequence 635, App
C 45	63.8	1.4	744802	12	US-10-292-798-1369	Sequence 1369, Ap

ALIGNMENTS

RESULT 1

US-09-922-217-343/c  
; Sequence 343, Application US/09922217  
; Patent No. US20020076414A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Secrist, Heather  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Meagher, Madeleine Joy  
; APPLICANT: Stolk, John A.  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Smith, Carole Lynn  
; APPLICANT: Wang, Aijun  
; APPLICANT: Clapper, Jonathan D.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS  
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE  
; FILE REFERENCE: 210121.471C13  
; CURRENT APPLICATION NUMBER: US/09/922.217  
; CURRENT FILING DATE: 2001-08-03  
; NUMBER OF SEQ ID NOS: 1124  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 343  
; LENGTH: 646  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-922-217-343

Query Match	12.5%	Score 552.2;	DB 9;	Length 646;
Best Local Similarity	93.0%	Pred. No. 2.6e-110;		
Matches	609;	Conservative	4;	Mismatches 32;
				Indels 10; Gaps 3;
Qy	3419	AAAGCTTTCAGCCCTTCCTAGGACAGAGAAATGGGTAGCCCAATCTGCAATTTCTACT	3478	
Db	645	AAAGCTTTCAGCCCTTCCTAGGACAGAGAAATGGGTAGCCCAATCTGCAATTTCTACT	586	

BEST AVAILABLE COPY

QY 3479 ACAGGCAATTGAGACCAAGTGTAGATTGAAATATATATAGAGAGTTATGAACACATTAAATT 3538  
DB |||||||  
DB 585 ACAGGCAATTGAGACCAAGTGTAGATTGAAATATATATAGAGAGTTATGAACACATTAAATT 526  
QY 3539 ATGATAGTGTATGACATTTGGATAGACATGGGATACCTTTAGAGTAGAATTGACAGGGC 3598  
DB |||||||  
DB 525 ATGATAGTGTATGACATTTGGATAGACATGGGATACCTTTAGAGTAGAATTGACAGGGC 466  
QY 3599 ATATTAGTGTATGAAATGGAGTCAATTTGAGTCTVTTAATAGCCATGATCAATAATTACCA 3658  
DB |||||||  
DB 465 ATATTAGTGTATGAAATGGAGTCAATTTGAGTCTCTTAATAGCCATGATCAATAATTACCA 406  
QY 3659 AGTGAAGCTGGTGGAAACATATAGGTCCTCCATTTTACAGTTAAGGAATATAATGGACAGATT 3718  
DB |||||||  
DB 405 AGTGAAGCTGGTGGAAACATATAGGTCCTCCATTTTACAGTTAAGGAATATAATGGACAGATT 346  
QY 3719 AATATTGTTTCTGTCATGCCCAATCCCTTTCTAAGGAAGACTGCCCTACTATAGCAG 3778  
DB |||||||  
DB 345 AATATTGTTTCTGTCATGCCCAATCCCTTTCTAAGGAAGACTGCCCTACTATAGCAG 286  
QY 3779 TTTTATATTGTCATTTATGAATATATGAATGAGGAGTCTGTTACCTCCTGTCCTTT 3838  
DB |||||||  
DB 285 TTTTATATTGTCATTTATGAATATATGAATGAGGAGTCTGTTACCTCCTGTCCTTT 227  
QY 3839 ACAATATTGGTGTGTCATGCCCAATCCCTTTCTAAGGAAGACTGCCCTACTATAGCAG 3898  
DB |||||||  
DB 226 ACAATATTGGTGTGTCATGCCCAATCCCTTTCTAAGGAAGACTGCCCTACTATAGCAG 171  
QY 3899 AGGTGGATGTTTCCATTTGGGTTTAAATTTGATATCCCTGATAGCTATATTTGGGTGAT 3958  
DB |||||||  
DB 170 TGAAG-----TTTCAATTTGGTGTGTCATGCCCAATCCCTGATAGCTATATTTGGGTGAT 116  
QY 3959 AGAATTTCTTTATACATTTAGATCAAGTCTCTTGYCGGATATACGTTATGAGATATTA 4018  
DB |||||||  
DB 115 AGAATTTCTTTATACATTTAGATCAAGTCTCTTGYCGGATATATGTTATGAGATATTA 56  
QY 4019 CACCTAGTCTGGGCTGACGTTTCTTTATGCTTTTGTATGATGAAGATTTT 4073  
DB |||||||  
DB 55 CACCTAGTCTGGGCTGACGTTTCTTTATGCTTTTGTATGATGAAGATTTT 1

RESULT 2  
US-09-833-263-343/c  
; Sequence 343, Application US/09833263  
; Patent No. US20020110547A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Aijun  
; APPLICANT: Clapper, Jonathan D.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Meagher, Madeleine J.  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND  
; FILE REFERENCE: 210121.471C12  
; CURRENT APPLICATION NUMBER: US/09/833,263  
; CURRENT FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 343  
; LENGTH: 646  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-833-263-343

Query Match 12.5%; Score 552.2; DB 10; Length 646;  
Best Local Similarity 93.0%; Pred. No. 2.6e-110;  
Matches 609; Conservative 4; Mismatches 32; Indels 10; Gaps 3;  
QY 3419 AAAAGCTTCTCAGGCTTCCCTAGGGAACAGAAATTTGGGTAGGCAATCTGCAATTTCTACT 3478  
DB |||||||  
DB 645 AAAAGCTTCTCAGGCTTCCCTAGGGAACAGAAATTTGGGTAGGCAATCTGCAATTTCTACT 586  
QY 3479 ACAGGCAATTGAGACCAAGTGTAGATTGAAATATATATAGAGAGTTATGAACACATTAAATT 3538  
DB |||||||

DB 585 ACAGGCAATTGAGACCAAGTGTAGATTGAAATATATATAGAGAGTTATGAACACATTAAATT 526  
QY 3539 ATGATAGTGTATGACATTTGGATAGACATGGGATACCTTTAGAGTAGAATTGACAGGGC 3598  
DB |||||||  
DB 525 ATGATAGTGTATGACATTTGGATAGACATGGGATACCTTTAGAGTAGAATTGACAGGGC 466  
QY 3599 ATATTAGTGTATGAAATGGAGTCAATTTGAGTCTVTTAATAGCCATGATCAATAATTACCA 3658  
DB |||||||  
DB 465 ATATTAGTGTATGAAATGGAGTCAATTTGAGTCTCTTAATAGCCATGATCAATAATTACCA 406  
QY 3659 AGTGAAGCTGGTGGAAACATATAGGTCCTCCATTTTACAGTTAAGGAATATAATGGACAGATT 3718  
DB |||||||  
DB 405 AGTGAAGCTGGTGGAAACATATAGGTCCTCCATTTTACAGTTAAGGAATATAATGGACAGATT 346  
QY 3719 AATATTGTTTCTGTCATGCCCAATCCCTTTCTAAGGAAGACTGCCCTACTATAGCAG 3778  
DB |||||||  
DB 345 AATATTGTTTCTGTCATGCCCAATCCCTTTCTAAGGAAGACTGCCCTACTATAGCAG 286  
QY 3779 TTTTATATTGTCATTTATGAATATATGAATGAGGAGTCTGTTACCTCCTGTCCTTT 3838  
DB |||||||  
DB 285 TTTTATATTGTCATTTATGAATATATGAATGAGGAGTCTGTTACCTCCTGTCCTTT 227  
QY 3839 ACAATATTGGTGTGTCATGCCCAATCCCTTTCTAAGGAAGACTGCCCTACTATAGCAG 3898  
DB |||||||  
DB 226 ACAATATTGGTGTGTCATGCCCAATCCCTTTCTAAGGAAGACTGCCCTACTATAGCAG 171  
QY 3899 AGGTGGATGTTTCCATTTGGGTTTAAATTTGATATCCCTGATAGCTATATTTGGGTGAT 3958  
DB |||||||  
DB 170 TGAAG-----TTTCAATTTGGTGTGTCATGCCCAATCCCTGATAGCTATATTTGGGTGAT 116  
QY 3959 AGAATTTCTTTATACATTTAGATCAAGTCTCTTGYCGGATATACGTTATGAGATATTA 4018  
DB |||||||  
DB 115 AGAATTTCTTTATACATTTAGATCAAGTCTCTTGYCGGATATATGTTATGAGATATTA 56  
QY 4019 CACCTAGTCTGGGCTGACGTTTCTTTATGCTTTTGTATGATGAAGATTTT 4073  
DB |||||||  
DB 55 CACCTAGTCTGGGCTGACGTTTCTTTATGCTTTTGTATGATGAAGATTTT 1

RESULT 3  
US-10-025-380-343/c  
; Sequence 343, Application US/10025380  
; Publication No. US20020182191A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Secrist, Heather  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Meagher, Madeleine Joy  
; APPLICANT: Stolk, John A.  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Jiang, Xuqiu  
; APPLICANT: Smith, Carole L.  
; APPLICANT: King, Gordon E.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Clapper, Jonathan D.  
; APPLICANT: Skeiky, Yasir A. W.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darriek  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS  
; FILE REFERENCE: 210121.471C14  
; CURRENT APPLICATION NUMBER: US/10/025,380  
; CURRENT FILING DATE: 2001-12-19  
; NUMBER OF SEQ ID NOS: 1129  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 343  
; LENGTH: 646  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-025-380-343



## BEST AVAILABLE COPY

QY 3190 AGAAGTGAAGAAATGGAACAGTGAAGAAATGAGGCAATATTTCCATGACTTCCCTGTAA 3249  
Db 61 AGAAGTGAAGAAATGGAACAGTGAAGAAATGAGGCAATATTTCCATGACTTCCCTGTAA 120  
QY 3250 ACAGAGCAACAGAGGACAGAGGCTGGCTCTACATCTCTACCTTCCAAATCTT 3309  
Db 121 ACAGAGCAACAGAGGACAGAGGCTGGCTCTACATCTCTACCTTCCAAATCTT 180  
QY 3310 GTGGAAGTGCATCTACTTCCAGAACCAAAATTAATCTTCTCAAGTCTGGCTGTTC 3369  
Db 181 GTGGAAGTGCATCTACTTCCAGAACCAAAATTAATCTTCTCAAGTCTGGCTGTTC 240  
QY 3370 AGGTGGAATCCAGTCTCAAGGAGTTAGGAAATGAAGGCTTTTAAAAAGCTTCTC 3429  
Db 241 AGGTGGAATCCAGTCTCAAGGAGTTAGGAAATGAAGGCTTTTAAAAAGCTTCTC 300  
QY 3430 AGCTTCTCAGGACAGAAATGGGTGAGCAATCTGCAATTTCTACTACAGGCATTTGA 3489  
Db 301 AGCTTCTCAGGACAGAAATGGGTGAGCAATCTGCAATTTCTACTACAGGCATTTGA 360  
QY 3490 GACCAAGTTAGATTTGAAATATTTATAGAGGTTATGAACATTTAAATTTATGATAGTGT 3549  
Db 361 GACCAAGTTAGATTTGAAATATTTATAGAGGTTATGAACATTTAAATTTATGATAGTGT 420  
QY 3550 ATGACATTTGATAGAAATGGAATCTTTAGAGTGAATTTGACAGGCATTTAGTTGA 3609  
Db 421 ATGACATTTGATAGAAATGGAATCTTTAGAGTGAATTTGACAGGCATTTAGTTGA 480  
QY 3610 TGAATGGAGTCTTTGAGTCTTTTAAATAGCCATGTATCATATAATTTACCAAGTGAAGCTGG 3669  
Db 481 TGAATGGAGTCTTTGAGTCTTTTAAATAGCCATGTATCATATAATTTACCAAGTGAAGCTGG 540  
QY 3670 T 3670  
Db 541 T 541

## RESULT 6

US-10-146-502-1737  
; Sequence 1737, Application US/10146502  
; Publication No. US20030069180A1  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Secrist, Heather  
; APPLICANT: Wang, Aijun  
; APPLICANT: Stolk, John A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.527C2  
; CURRENT APPLICATION NUMBER: US/10/146.502  
; CURRENT FILING DATE: 2002-05-14  
; NUMBER OF SEQ ID NOS: 2241  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1737  
; LENGTH: 541  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-146-502-1737

Query Match 12.2%; Score 537.4; DB 15; Length 541;  
Best Local Similarity 99.4%; Pred. No. 4e-107;  
Matches 538; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3130 ACCGTGTATCCAGCAAGAGGAGTCCAGTCAAGAGTCACTACAACTGATTTGTTT 3189  
Db 1 ATCTGTATCCAGCAAGAGGAGTCCAGTCAAGAGTCACTACAACTGATTTGTTT 60  
QY 3190 AGAAGTGAAGAAATGGAACAGTGAAGAAATGAGGCAATATTTCCATGACTTCCCTGTAA 3249  
Db 61 AGAAGTGAAGAAATGGAACAGTGAAGAAATGAGGCAATATTTCCATGACTTCCCTGTAA 120  
QY 3250 ACAGAGCAACAGAGGACAGAGGCTGGCTCTACATCTCTACCTTCCAAATCTT 3309

Db 121 ACAGAGCAACAGAGGACAGAGGCTGGCTCTACATCTCTACCTTCCAAATCTT 180  
QY 3310 GTGGAAGTGCATCTACTTCCAGAACCAAAATTAATCTTCTCAAGTCTGGCTGTTC 3369  
Db 181 GTGGAAGTGCATCTACTTCCAGAACCAAAATTAATCTTCTCAAGTCTGGCTGTTC 240  
QY 3370 AGGTGGAATCCAGTCTCAAGGAGTTAGGAAATGAAGGCTTTTAAAAAGCTTCTC 3429  
Db 241 AGGTGGAATCCAGTCTCAAGGAGTTAGGAAATGAAGGCTTTTAAAAAGCTTCTC 300  
QY 3430 AGCTTCTCAGGACAGAAATGGGTGAGCAATCTGCAATTTCTACTACAGGCATTTGA 3489  
Db 301 AGCTTCTCAGGACAGAAATGGGTGAGCAATCTGCAATTTCTACTACAGGCATTTGA 360  
QY 3490 GACCAAGTTAGATTTGAAATATTTATAGAGGTTATGAACATTTAAATTTATGATAGTGT 3549  
Db 361 GACCAAGTTAGATTTGAAATATTTATAGAGGTTATGAACATTTAAATTTATGATAGTGT 420  
QY 3550 ATGACATTTGATAGAAATGGAATCTTTAGAGTGAATTTGACAGGCATTTAGTTGA 3609  
Db 421 ATGACATTTGATAGAAATGGAATCTTTAGAGTGAATTTGACAGGCATTTAGTTGA 480  
QY 3610 TGAATGGAGTCTTTGAGTCTTTTAAATAGCCATGTATCATATAATTTACCAAGTGAAGCTGG 3669  
Db 481 TGAATGGAGTCTTTGAGTCTTTTAAATAGCCATGTATCATATAATTTACCAAGTGAAGCTGG 540  
QY 3670 T 3670  
Db 541 T 541

## RESULT 7

US-10-102-524-532  
; Sequence 532, Application US/10102524  
; Publication No. US20030109434A1  
; GENERAL INFORMATION:  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Gordon, Brian  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; FILE REFERENCE: 210121.572  
; CURRENT APPLICATION NUMBER: US/10/102.524  
; CURRENT FILING DATE: 2002-03-19  
; NUMBER OF SEQ ID NOS: 1863  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 532  
; LENGTH: 587  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-102-524-532

Query Match 11.5%; Score 507; DB 15; Length 587;  
Best Local Similarity 93.6%; Pred. No. 1.8e-100;  
Matches 559; Conservative 4; Mismatches 24; Indels 10; Gaps 3;

QY 3419 AAAAGCTTCTCAGCCTTCTTAGGGAAACAGAAATTTGGGTGAGCCAAATCTGCAATTTCTACT 3478  
Db 1 AAAAGCTTCTCAGCCTTCTTAGGGAAACAGAAATTTGGGTGAGCCAAATCTGCAATTTCTACT 60  
QY 3479 ACAGGCATTTGAGACCAAGTATTTGAAATATTTATAGAGGTTATGAACACTTAAAT 3538  
Db 61 ACAGGCATTTGAGACCAAGTATTTGAAATATTTATAGAGGTTATGAACACTTAAAT 120  
QY 3539 ATCATAGTGGTATGACATTTGGATAGAACATGGGATCTTTTAGAAGTAGAATTCACAGGC 3598  
Db 121 ATCATAGTGGTATGACATTTGGATAGAACATGGGATCTTTTAGAAGTAGAATTCACAGGC 180  
QY 3599 ATATTAGTGTGAAATGAGTCAATTTGAGTCTTTTAAATAGCCATGTATCATATAATTTACCA 3658

Db 181 ATATTAGTTGATGAATGGAGTCATTTGAGTCTCTTAATAGCCATGTATCATTAATTACCA 240  
Qy 3659 AGTGAAGCTGGTGAACATATGGTCTCCATTTTACAGTTAAGGAATATAATGGACAGATT 3718  
Db 241 AGTGAAGCTGGTGAACATATGGTCTCCATTTTACAGTTAAGGAATATAATGGACAGATT 300  
Qy 3719 AATATTGTTTCTGTGATGCCCAATCCCTTTCTAAGGAAGACTGCCCTACTATAGCAG 3778  
Db 301 AATATTGTTTCTGTGATGCCCAATCCCTTTCTAAGGAAGACTGCCCTACTATAGCAG 360  
Qy 3779 TTTTATATTGTCATTTATGAATATAAATGAATGAGGAGTTCTGTGACCTCTGTCTTT 3838  
Db 361 TTTTATATTGTCATTTATGAATATAAATGAATGAATGA-GAGTTCTGGTACCTCTGTCTTT 419  
Qy 3839 ACAAATATGGGTGTTGTCAGATATTTTCCCTTTTAAACMTTCCCAATTCGGGTGTGT 3898  
Db 420 ACAAATATGG- - -TGTGTGACGATATTTTCCCTTTTAAACCATTCCTCAATCGGTGTGTAG 475  
Qy 3899 AGGTGGATGTTCCATTTGGTGTATTTTATTTGTATATCCCTGATAGCTATTAATGGGTGAT 3958  
Db 476 TGATG- - -TTTCATTTTGGTGTATTTTAAATTTGTATATCCCTGATAGCTATAATTTGGGTGAT 530  
Qy 3959 AGAAATCTTTATACATCTAGATGCAAGTCTCTTGYCGGATATACGTATTTGAGATA 4015  
Db 531 AGAAATCTTTATACATCTAGATGCAAGTCTCTTGYCGGATATATGTATTTGAGATA 587

RESULT 8  
US-09-918-995-13834  
; Sequence 13834, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 13834  
; LENGTH: 468  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(468)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-13834

Query Match 9.28; Score 405.6; DB 11; Length 468;  
Best Local Similarity 97.4%; Pred. No. 2.3e-78;  
Matches 411; Conservative 1; Mismatches 10; Indels 0; Gaps 0;  
Qy 2938 TGGTCTTACTAGCTGGGTGCTGTGTTGAGCTTATTTAGAGCTTAGTTTTCCTA 2997  
Db 47 TCGTCTTACTAGCTGGGTGCTGTGTTGAGCTTATTTAGAGCTTAGTTTTCCTA 106  
Qy 2998 CTTATAAGTAGAATGGTGAGATTTTCTTTTCTACCKTAAAGGGAGATGGTAAGA 3057  
Db 107 CTTATAAGCAGAAACGGGAGATTTGTTTCTACCTTAAAGGAGATGGCAAGA 166  
Qy 3058 AACATGAATGTCCTTTTTCAACTTTATTTGACAAAGTATTTTCAAGTCTGTGTTCAAAA 3117  
Db 167 AACAAATGAATGTCCTTTTTCAACTTTATTTGACGAGTGAATTTTCAAGTCTGTGTTCAAAA 226  
Qy 3118 ATATATTGATGCTGCTGTATCCAGCAAGAGGAGTTCCAGTCAAGAGTCACTTACAACT 3177  
Db 227 ATATATTGATGCTGCTGTATCCAGCAAGAGGAGTTCCAGTCAAGAGTCACTTACAACT 286  
Qy 3178 GATTAGTTGTTTAGAATGGAATGGAACAGTGGAGGAATGGAGGCCATATTTTCCATGA 3237

Db 287 GATTAGTTGTTTAAAGAAATGAGAAATGGAACAGTGGAGGAATGAGGCCATATTTTCCATGA 346  
Qy 3238 CTTCCCTTTTAAACAGAACAGAACAGAGGAGGCTGGCTCTTACATCACTCTCAC 3297  
Db 347 CTTCCCTTTTAAACAGAACAGAACAGAGGAGGCTGGCTCTTACATCACTCTCAC 406  
Qy 3298 CTTCCAAATCTTGGGAAGTGCATCTACTTTGCCAGAACCAAAATTAACCTTACTTCCAAAGTT 3357  
Db 407 CTTCCAAATCTTGGGAAGTGCATCTACTTTGCCAGAACCAAAATTAACCTTACTTCCAAAGTT 466  
Qy 3358 CT 3359  
Db 467 CT 468

RESULT 9  
US-09-783-590-3449  
; Sequence 3449, Application US/09783590  
; Patent No. US20020110850A1  
; GENERAL INFORMATION:  
; APPLICANT: Dillon, Patrick J.  
; APPLICANT: Haseltine, William A.  
; APPLICANT: Li, Haodong  
; APPLICANT: Rosen, Craig A.  
; APPLICANT: Ruben, Steven M.  
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2  
; FILE REFERENCE: PO-16,2C1  
; CURRENT APPLICATION NUMBER: US/09/783,590  
; CURRENT FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 08/420,856  
; PRIOR FILING DATE: 1995-04-12  
; PRIOR APPLICATION NUMBER: 08/346,731  
; PRIOR FILING DATE: 1994-11-21  
; NUMBER OF SEQ ID NOS: 12485  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3449  
; LENGTH: 360  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (115)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (164)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (251)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (301)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (320)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (324)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (327)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (328)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (329)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (359)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-783-590-3449

## Page 6

Db	121	TATCTGAGATGAGCTGTGGACAAACTCAGACAATAACTTATTTCAGATACAGATT	180
QY	1635	TAAATCTATTGTGAAAAATTCGCCAGTAAATCTCATGCTGCAGAAAAAGCTTAAGATCAA	1694
Db	181	TAAATCTATTGTGAAAAATTCGCCAGTAAATCTCATGCTGCAGAAAAAGCTTAAAAAAA	240
QY	1695	ATAAAAAAAGGG	1706
Db	241	ANAAANGGGGG	252

```

; SOFTWARE: PERL Program
; SEQ ID NO 5167
; LENGTH: 272
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030237110A9 700456477H1
; NAME/KEY: unsure
; LOCATION: 91, 242, 246, 256, 258, 260, 267, 270
; OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-5167

```

Ddb 191 TAAATCTATTGTGAAAAATTTGCCAGTAAATCTCATGCTGCAGAAAAGCTAAAAAAA 240  
 QY 1695 ATAAAAAAGGG 1706  
 Ddb 241 ANAAANGGGGG 252

RESULT 12  
 US-09-917-800A-803/c  
 ; Sequence 803, Application US/09917800A  
 ; Patent No. US20020119462A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mendrick, Donna  
 ; APPLICANT: Porter, Mark





